

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 19:33:26 ; Search time 51 Seconds
(without alignments)
989.707 Million cell updates/sec

Title: US-10-024-806-2

Perfect score: 1560

Sequence: 1 MATAATAAAVSSPAARG.....NPAASYMTGVLTIDGMVM 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1093	70.1	315	17 AAR89323	Rape leaf beta-ket
2	1093	70.1	315	17 AAR89322	Rape seed beta-ket
3	984	63.1	308	21 AAG35504	Arabidopsis thalia
4	981.5	62.9	267	21 AAG35505	Arabidopsis thalia
5	838	53.7	273	21 AAG40275	Arabidopsis thalia
6	835.5	53.6	232	21 AAG40276	Arabidopsis thalia
7	717.5	46.0	248	21 AAY54422	Amino acid sequenc
8	686.5	44.0	247	23 ABB48892	Listeria monocytog
9	676.5	43.4	165	21 AAG35506	Arabidopsis thalia

10	661.5	42.4	244	24 ABU18966	Pathogen specific
11	658.5	42.2	246	21 AAB15707	Staphylococcus aur
12	658.5	42.2	246	22 AAU33965	Staphylococcus aur
13	658.5	42.2	246	22 AAU33965	Staphylococcus aur
14	658.5	42.2	246	22 AAU37210	Staphylococcus aur
15	658.5	42.2	246	22 AAU37507	Staphylococcus aur
16	658.5	42.2	246	22 AAE02195	S. aureus NADPH-de
17	647.5	41.5	249	23 ABP39980	Staphylococcus epi
18	612.5	39.3	243	23 ABB54087	Lactococcus lactis
19	598.5	38.4	245	22 AAU35328	Enterococcus faeca
20	597.5	38.3	243	19 AAW80670	S. pneumoniae fatt
21	597.5	38.3	243	21 AAB15706	Streptococcus pneu
22	597.5	38.3	243	22 AAU37767	Streptococcus pneu
23	597.5	38.3	243	22 AAU37988	Streptococcus pneu
24	596.5	38.2	243	22 AAW01032	CFE 35 protein seq
25	596.5	38.2	243	24 ABU00775	S. pneumoniae type
26	587.5	37.7	243	23 ABP27345	Streptococcus poly
27	580.5	37.2	244	23 ABP28011	Streptococcus poly
28	576.5	37.0	244	21 AAY54421	Amino acid sequenc
29	576.5	37.0	244	22 AAU34533	E. coli cellular p
30	573.5	36.8	244	23 ABU10969	Poly3-hydroxybutan
31	573.5	36.8	244	23 ABB96548	Human short chain
32	556	35.6	247	21 AAB03794	3-ketoacyl-ACP red
33	556	35.6	247	22 AAU36300	Pseudomonas aerugi
34	555	35.6	282	24 ABP77406	N. gonorrhoeae ami
35	545.5	35.0	242	22 AAU35381	Haemophilus influe
36	530.5	34.0	248	20 AAY36959	Chlamydia trachoma
37	529	33.9	247	21 AAY95746	Bacillus megaterium
38	528	33.8	251	20 AAY34891	Chlamydia pneumonia
39	500.5	32.1	240	23 ABP27344	Streptococcus poly
40	499.5	32.0	171	22 AAG82281	S. epidermidis ope
41	496.5	31.8	247	20 AAW90010	Expressed antigen
42	496.5	31.8	247	22 AAU35749	Helicobacter pylor
43	488	31.3	248	20 AAW89908	Antigen 1 from clu
44	488	31.3	254	23 ABB31755	Protein with hydro
45	487.5	31.2	241	12 AAR10679	Acetoacetyl CoA re

ALIGNMENTS

RESULT 1

AAR89323

ID AAR89323 standard; Protein; 315 AA.

XX

AC AAR89323;

XX

DT 13-APR-1996 (first entry)

XX

DE Rape leaf beta-ketoacyl-ACP-ketoreductase.

XX

KW Rape; leaf; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase;

KW plasmid pJR16.2; cDNA library; Escherichia coli; vector;

KW plasmid; stroma; transit peptide; cassette; antisense; oilseed;

KW transgenic plant; crop improvement; lipid; metabolic engineering;

KW polymer; rapeseed oil.

XX

OS Brassica napus.

XX

PH Key Location/Qualifiers

FT Peptide 1..55

FT /note= "transit peptide"

XX

PN WO9602652-A2.

XX

PD 01-FEB-1996.

XX

PF 17-JUL-1995; 95WO-GB01678.

XX

PR 20-JUL-1994; 94GB-0014622.

XX

PA (ZENE) ZENECA LTD.

XX

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PI Chose D, Elborough K, Pentem PA, Slabas AR, White A;
XX WPI; 1996-105914/11.
DR N-PSDB; AAQ99305.
XX
XX New isolated rape beta-ketoreductase DNA - used to develop plants
PT with lower or higher oil contents or with altered oil compsn.
XX
XX Claim 2; Page 16; 29pp; English.
XX
XX The sequence corresponds to a rape leaf beta-ketoreductase encoded
CC by a cDNA insert in plasmid pUR5.2 in Escherichia coli XL1-Blue.
CC A plastid stroma targeting transit peptide is present. DNA
CC encoding the protein may be inserted in a vector or expression
CC cassette in sense or antisense orientation for expression in an
CC oilseed plant, e.g. for production of transgenic rape plants with
CC low or modified oil content, diversion of metabolism to alternative
CC storage compounds, e.g. starch, protein or engineered polymers, or
CC production of plants with enhanced oil content. The DNA may also
CC be used as a probe to obtain similar genes from other plants. The
CC transit peptide may be used to direct other proteins to leaf
CC plastids.
XX
SQ Sequence 315 AA;
Query Match 70.1%; Score 1093; DB 17; Length 315;
Best Local Similarity 80.7%; Pred. No. 5.1e-80;
Matches 213; Conservative 28; Mismatches 23; Indels 0; Gaps 0;
Qy 55 VOTHVAVEQAVVKDQATKLEAPVVTGASRGIGKATALGKAGCKVLVNYARSSKEAE 114
Db 52 VKAQTAVEQSTGEAVPKVESPVVVTGASRGIGKATALGKAGCKVLVNYARSSKEAE 111
Qy 115 EVSKEIASGGEAITFGGDSKEADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRMK 174
Db 112 EVSKEIASGGEAITFGGDSKEADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRMK 171
Qy 175 SQWODVIDLNLGTGVFLCTQATKVMKKRKKIINIASVGLTGNVGOANYSAKAGVIG 234
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Qy 235 FTKTVAREYASRNINVAIAPGFIASDMTAELEKILSTIPLGRYGQPEEVAGLVE 294
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RESULT 2
AAR89322
ID AAR89322 standard; Protein; 315 AA.
XX
XX AAR89322;
XX
XX 13-APR-1996 (first entry)
XX
XX Rape seed beta-ketoacyl-ACP-ketoreductase.
XX
XX Rape, seed; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase;
KW plasmid pUR5.10.1; cDNA library; embryo; Escherichia coli; vector;
KW plastid; stroma; transit peptide; cassette; antisense; oilseed;
KW transgenic plant; crop improvement; lipid; metabolic engineering;
KW polymer; rapeseed oil.
XX
XX Brassica napus.
XX
XX Key Location/Qualifiers
FH Peptide 1..56
FT /note= "transit peptide"
XX
XX WO9602652-A2.

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OS	Arabidopsis thaliana.	
XX	EP1033405-A2.	
XX	06-SEP-2000.	
XX	25-FEB-2000; 2000EP-0301439.	
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XX	05-MAR-1999;	99US-0121180.
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QY	61	AVEQAVVKDATKLEAPVVVVTGARGTGKATALALGKAGCKVLVNYARSSKEAEVSKEI 120
Db	62	ATEQSPGEVVKVESPVVITGASRGIGKATALALGKAGCKVLVNYARSAKEAEVAKQI 121
QY	121	EASGEALTFGDYSKEADVESMMKALDKWGTIDVNNAGITRDTLLMEMKKSQWQDV 180
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QY	181	IDLNLITGVFLCTQATKVMKKRKGIINIASVVGLTGNVGQANYSAKAGVIGFTKIVA 240
Db	182	IALNLTGVFLCTQ-----GRINISSVGLIGNIQANVAAKGVISFSKTA 230
QY	241	REYASRNINVAIPGFTASDWTALGEELEKKILSTIPLGRYQOPHEVAGLVEFLALNP 300
Db	231	REGASRNINNVVCPGFTASDWTALGEDMEKKILGTIPLGRYKAEVAGLVEFLALSP 290
QY	301	AASYMTGQVLTIDGGMV 318
Db	291	AASVITGQAFITDGGIAI 308


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Query Match 62.9%; Score 981.5; DB 21; Length 267;
Best Local Similarity 72.3%; Pred.No. 4e-71;
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QY 165 RDTLLMRKMSQWQVDIDLNLGTGVLCTQAAATKVMKKKGGKILINIASVVGTLGNVGOAN 224
Db 125 RDTLLMRKMSQWQVDIENLNLGTGVLCTQAAATKVMKKKGGKILINIASVVGTLGNVGOAN 173
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Db      174 YAAKGGVISFSKTAAREGASRNINNVVCPGFASDMTAEELGDEMEKKILGTIPLGRYG 233
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RESULT 5
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AC AAG40275;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 49950.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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DB 2 AAATAAPRLISLKAVAKLGFREISQIRQLAPLHSAIPHFGMLRCKRSQPFSTSVKQAT 61

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61 AVEQAVVKDAKLEAPVVVVVTGASRGIGKATAGKAGCKVLVNYARSSKEAEVSKEI 120
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121 EASGGEAITFGGDYSKEADVSMKKAALDKWGTIDVLVNNAGITRDTLLMRMKSQWQDV 180
122 EYGGQAITFGGDYSKATDVEDAMKATLDKWGTIDVVVNNAGITRDTLLMRMKSQWQDV 181
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182 TALNLTVGLCTQ-----GRIINISVVLGICNIGQANYAAAKGGVISPSTAA 230
241 REYASRNINVAIAPGFIAADMTAELEKELKILSTIPLG 281
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XX DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 49951.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 28-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match      53.6%; Score 835.5; DB 21; Length 232;
Best Local Similarity 71.7%; Pred. No. 28-59;
Matches 170; Conservative 25; Mismatches 29; Indels 13; Gaps 2;

QY 47 RSGRFGSG--VQTHVAAVQAVVVDKATLEAFVVTGASRGIGKATLALGKAGCKVLV 104
DB 5 RSRQPFSTSVKQAQATATQSPGEVQVKVESPVVITGASRGIGKATLALGKAGCKVLV 64
QY 105 NYARSSKEAEVYSKEIABGGAITFGDVSKEADVESMMKAALDKWGTIDVLVNNAGIT 164
DB 65 NYARSAKEAEVVAKQIEEYGGQAITFGDVSKEADVESMMKAALDKWGTIDVLVNNAGIT 124
QY 165 RTLLMRMKKSQWQDVLDLNLGTVFLCTQATKVMKMKKGIINIASVVTGTVNNGQAN 224
DB 125 RTLLMRMKKSQWQDVLDLNLGTVFLCTQ-----GRINISSVVGIGNIGQAN 173
QY 225 YSAKAGVIGFTKTVAREYASRNINVAIAPGFIASDMTAELEGELEKKILSTIPIG 281
DB 174 YAAKGGVISFSTAAAREGASRNINVVVCPGFIASDMTAELEGELEKKILSTIPIG 230

RESULT 7
ID AAY54422 standard; Protein; 248 AA.
XX AAY54422;
AC AAY54422;
XX
DT 06-APR-2000 (first entry)
XX
DE Amino acid sequence of a beta-ketoacyl-ACP reductase protein.
XX
KW Beta-ketoacyl-ACP reductase; Type II fatty acid synthetase;
KW stereoselectivity; 4-chloroacetoacetic acid ester;
KW (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;
KW beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;
KW polybeta-hydroxy fatty acid biosynthesis; optically active;
KW 4-halo-3-hydroxybutyric acid ester.
XX
OS Bacillus subtilis.
XX
PN EP955375-A2.
XX
PD 10-NOV-1999.
XX
PF 10-MAY-1999; 99EP-0109403.
XX
PR 08-MAY-1998; 98JP-0126507.
PR 21-OCT-1998; 98JP-0300178.
PR 05-APR-1999; 99JP-0098205.
XX
PA (DAIL ) DAICEL CHEM IND LTD.
XX
PI Yamamoto H;
XX
XX WPI; 2000-118183/11.
DR N-PSDB; AA245749.
XX
PT Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -
XX
PS Claim 6; Page 19-20; 34pp; English.
XX
CC The present sequence represents a beta-ketoacyl-ACP reductase protein
CC of Bacillus subtilis. The beta-ketoacyl-ACP reductase enzyme constitutes
CC a Type II fatty acid synthetase. The enzyme has an extremely high
CC reducing activity and stereoselectivity towards 4-chloroacetoacetic
CC acid ester. The specification describes a method for producing a
CC (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
CC asymmetrically reducing 4-halo-acetoacetic acid ester or its
CC derivative with beta-ketoacyl-acyl carrier protein reductase
CC constituting Type II fatty acid synthase, or acetoacetyl-CoA
CC reductase constituting the polybeta-hydroxy fatty acid biosynthesis
CC system. The novel method is used to produce optically active
```

```
CC 4-halo-3-hydroxybutyric acid ester, with a high purity.
XX
SQ Sequence 248 AA;
Query Match      46.0%; Score 717.5; DB 21; Length 248;
Best Local Similarity 57.3%; Pred. No. 6.8e-50;
Matches 141; Conservative 47; Mismatches 57; Indels 1; Gaps 1;

QY 73 LEAPVVVTGASRGIGKATLALGKAGCKVLVNYARSSKEAEVYSKEIABGGAITFGG 132
DB 4 LNDKTAIYTGASRGIGRSIALALAKSGANVVVNYSGNEAKANEVVEDEIKSMGRKAIVKA 63
QY 133 DVSKEADVESMMKAALDKWGTIDVLVNNAGITRDLLMRMKKSQWQDVLDLNLGTVFLCT 192
DB 64 DVSNEPDVQNMKLTSLVFSFIDVLVNNAGITRDLLMRMKKEDEWDDVININLKGVFNCT 123
QY 193 QAAATKVMKMKKGIINIASVVTGTVNNGQANYSAAKAGVIGFTKTVAREYASRNINVA 252
DB 124 KAVTRQMMKQSGRIINVSIVGSGNPGQANYVAAKAGVIGLTKSSAKELASRNITVNA 183
QY 253 IAPGFIASDMTAELEGELEKKILSTIPIGRYGOPEEVAGLVFLALNPAASVMTQVLTI 312
DB 184 IAPGFIISTMDTKLAKQVQDEMLKQIPLARFGPESDVSVVTFLLA-SGARYMTQGTLLHI 242
QY 313 DGGVMV 318
DB 243 DGGVMV 248

RESULT 8
ID ABB48892 standard; Protein; 247 AA.
XX ABB48892;
AC ABB48892;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #1596.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-PR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP ) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
XX WPI; 2002-010914/01.
DR
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX and prevention of Listeria and related bacterial infections, and
XX related polypeptides
XX
PS Claim 6; SEQ ID No 1597; 192pp; French.
XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-g (see ABA03041). The genome sequence and fragments of
```


Meinke A, Nagy E, Von Ahnen U, Klade C, Henics T, Zauner W;


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QY 139 DVESMMKAALDKWGTIDVLVNNAGITRDTLLMRMKSQWQDVLDNLGTGFLCTQAAATKV 198
Db 68 EVKAMIKKEVWSQFGLDVLVNNAGITRDLNLMRKEQWDDVIDTNLKGVCNCTQKATPQ 127

QY 199 MMKRGKGIINIASVGLTGNVGOANYSAAGAGVIGFTKTAREVYASNNINNAIAPGFI 258
Db 128 MLRQSGAIINLSSVGVAGNPGQANYATKAGVIGLTKSAARELASRGITVNAVAPGFI 187

QY 259 ASDMTAELGEELEKILSTIPLGRYQGPVEEVAGLVEFLALNPAASYMTGQVLTIDGGMMV 318
Db 188 VSDMTDALSDDELKEQMLTQIPLARFGQDITANTVAFLA-SDKAKYITGTQTHVNGGMYM 246

RESULT 14
AAU37210
ID AAU37210 standard; Protein; 246 AA.
AC AAU37210;
XX
XX
DT 14-FEB-2002 (first entry)
DE Staphylococcus aureus cellular proliferation protein #1380.
KW Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US09180.
XX
XX PR 21-MAR-2000; 2000US-191078P.
XX PR 23-MAY-2000; 2000US-206848P.
XX PR 26-MAY-2000; 2000US-207727P.
XX PR 23-OCT-2000; 2000US-242578P.
XX PR 27-NOV-2000; 2000US-253625P.
XX PR 22-DEC-2000; 2000US-257931P.
XX PR 16-FEB-2001; 2001US-269308P.
XX
XX PA (ELIT-) ELITRA PHARM INC.
XX
XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX N-PSDB; AAS55069.
XX
XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX PS Example 3; Seq ID No 12803; 511pp; English.
XX
XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the
XX CC genes, their use in the discovery of novel antibiotics, the essential
XX CC genes themselves and the encoded proteins. The prokaryotes used are
XX CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX CC invention is also useful for the identification of potential new targets
XX CC for antibiotic development. The antisense nucleic acids can also be used
XX CC to identify proteins used in proliferation, to express these proteins,
XX CC and to obtain antibodies capable of binding to the expressed proteins.
XX CC The proteins can be used to screen compounds in rational drug discovery
XX CC programmes. The antisense nucleic acid sequence is also useful to screen
XX CC for homologous nucleic acids which are required for cell proliferation in
XX CC a wide variety of organisms. The present sequence represents an
XX CC essential prokaryotic cellular proliferation protein.
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at
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CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 246 AA;
XX
XX Query Match 42.2%; Score 658.5; DB 22; Length 246;
XX Best Local Similarity 55.0%; Pred No. 3.8e-45;
XX Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;

QY 79 VVTGASRGIGKATLALGAGCKVLVNYARSKAEAEVSEIEASGGEAITFGGDVSKEA 138
Db 8 LVTGASRGIGRSIALQAEEGYNVAVNYAGSKAEAVVEIKAKGVDSFAIQANVADAD 67

QY 139 DVESMMKAALDKWGTIDVLVNNAGITRDTLLMRMKSQWQDVLDNLGTGFLCTQAAATKV 198
Db 68 EVKAMIKKEVWSQFGLDVLVNNAGITRDLNLMRKEQWDDVIDTNLKGVCNCTQKATPQ 127

QY 199 MMKRGKGIINIASVGLTGNVGOANYSAAGAGVIGFTKTAREVYASNNINNAIAPGFI 258
Db 128 MLRQSGAIINLSSVGVAGNPGQANYATKAGVIGLTKSAARELASRGITVNAVAPGFI 187

QY 259 ASDMTAELGEELEKILSTIPLGRYQGPVEEVAGLVEFLALNPAASYMTGQVLTIDGGMMV 318
Db 188 VSDMTDALSDDELKEQMLTQIPLARFGQDITANTVAFLA-SDKAKYITGTQTHVNGGMYM 246

RESULT 15
AAU37507
ID AAU37507 standard; Protein; 246 AA.
AC AAU37507;
XX
XX DT 14-FEB-2002 (first entry)
DE Staphylococcus aureus cellular proliferation protein #1677.
KW Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US09180.
XX
XX PR 21-MAR-2000; 2000US-191078P.
XX PR 23-MAY-2000; 2000US-206848P.
XX PR 26-MAY-2000; 2000US-207727P.
XX PR 23-OCT-2000; 2000US-242578P.
XX PR 27-NOV-2000; 2000US-253625P.
XX PR 22-DEC-2000; 2000US-257931P.
XX PR 16-FEB-2001; 2001US-269308P.
XX
XX PA (ELIT-) ELITRA PHARM INC.
XX
XX PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX N-PSDB; AAS55366.
XX
XX PT New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX PS Example 3; Seq ID No 13100; 511pp; English.
XX
XX CC The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the
XX CC genes, their use in the discovery of novel antibiotics, the essential
XX CC genes themselves and the encoded proteins. The prokaryotes used are
XX CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
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OM protein - protein search, using sw model

Run on: November 7, 2003, 21:02:22 ; Search time 22 Seconds
(without alignments)
611.584 Million cell updates/sec

Title: US-10-024-806-2

Perfect score: 1560

Sequence: 1 MATRAATAAATAAAGVSPAARG.....NPAAASYMTGQVLTIDGGWVM 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pdp.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pdp.*

3: /cgn2_6/ptodata/1/iaa/5A COMB.pdp.*

4: /cgn2_6/ptodata/1/iaa/5B COMB.pdp.*

5: /cgn2_6/ptodata/1/iaa/PTCUS COMB.pdp.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1093	70.1	315	3	US-08-793-035-9
2	1093	70.1	315	3	US-08-793-035-9
3	658.5	42.2	246	3	US-09-238-481-2
4	658.5	42.2	246	4	US-09-572-810A-2
5	647.5	41.5	249	4	US-08-134-001C-4825
6	587.5	38.3	243	4	US-09-239-052-2
7	586.5	37.6	255	4	US-09-107-532A-4950
8	573.5	36.8	244	1	US-08-375-962B-13
9	573.5	36.8	244	2	US-08-562-114B-13
10	573.5	36.8	244	3	US-08-729-594A-13
11	573.5	36.8	244	4	US-08-937-933-13
12	565.5	36.2	362	4	US-08-252-991A-18645
13	528	33.8	251	4	US-09-198-452A-309
14	484.5	31.1	262	4	US-09-328-352-4761
15	479.5	30.7	241	4	US-08-178-257-19
16	467.5	30.0	158	4	US-09-724-623-85
17	466.5	29.9	273	6	5512669-4
18	461	29.6	186	4	US-08-858-207A-270
19	457	29.3	246	4	US-08-178-257-9
20	455	29.2	742	4	US-09-252-991A-24489
21	451	28.9	261	4	US-09-468-738A-29
22	451	28.9	261	4	US-09-940-019-29
23	451	28.9	261	4	US-09-940-037A-29
24	450	28.8	436	4	US-09-252-991A-26759
25	439.5	28.2	247	1	US-08-241-766-13
26	426.5	27.3	246	4	US-08-178-257-18
27	423.5	27.1	246	6	5229279-7

28	423.5	27.1	263	6	5229279-4
29	410	26.3	267	4	US-09-134-001C-5042
30	402.5	25.8	259	4	US-09-252-991A-28945
31	397	25.4	271	4	US-09-252-991A-18965
32	388	24.9	267	4	US-09-252-991A-32380
33	387	24.8	256	1	US-08-594-808B-7
34	385	24.7	263	4	US-09-134-001C-4512
35	384.5	24.6	274	4	US-09-134-001C-4431
36	384	24.6	275	4	US-09-107-532A-4805
37	383.5	24.6	267	4	US-09-773-748-1
38	380	24.4	262	4	US-09-328-352-5742
39	379.5	24.3	263	4	US-09-134-001C-3505
40	379	24.3	283	4	US-09-328-352-7773
41	377	24.2	251	4	US-09-648-004-20
42	376	24.1	456	4	US-09-252-991A-28323
43	374	24.0	303	4	US-09-634-955B-25
44	370.5	23.8	301	4	US-09-252-991A-24032
45	367.5	23.6	257	4	US-09-134-001C-3562

ALIGNMENTS

RESULT 1

US-08-793-035-9

; Sequence 9, Application US/08793035

; Patent No. 6011201

; GENERAL INFORMATION:

; APPLICANT: Slabas, Antoni R.

; APPLICANT: White, Andrew

; APPLICANT: Chase, Dianne

; APPLICANT: Elborough, Keiran

; APPLICANT: Fentem, Phillip A.

; TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From

; TITLE OF INVENTION: Brassica Napus

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: TX

; COUNTRY: US

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/793,035

; FILING DATE: 28-JUL-1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9414622.2

; FILING DATE: 20-JUL-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB95/01678

; FILING DATE: 17-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Kammerer, Patricia A.

; REGISTRATION NUMBER: 29,775

; REFERENCE/DOCKET NUMBER: MOBT:132

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713.787.1400

; TELEFAX: 713.787.1440

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 315 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-793-035-9

Query Match	70.1%;	Score 1093;	DB 3;	Length 315;
Best local Similarity	80.7%;	Pred. No. 1.6e-101;		
Matches 213;	Conservative 28;	Mismatches 23;	Indels 0;	Gaps 0;
Qy	55	VQTHVAVEQAVVDKAKLEAPVVVVTGASRGIGKATALALGKAGCKVLVNYARSKEAE	114	
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	:	:		
	:	:		
	:	:		
Db	52	VKAQATAVEQSTGEAPVKVESPVVVVTGASRGIGKATALSGLGAGCKVLVNYARSKEAE	111	
Qy	115	EVSKIEIASGCGEALTFFGSDVSEKADVESMMKAALDKGTIDVLVNNAGITDITLLMRKK	174	
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Db	112	EVSKQIEIYAGYQQAITFFGSDVSEKADVEAMMTAIDAWGTIIDVVVNNAGITDITLLMRKK	171	
Qy	175	SQMDVIDLNLITGVFLCTQAAATKVMKKRKGKIINIASVVGITGVNGOANYSAKAGVIG	234	
	:	:		
	:	:		
	:	:		
	:	:		
	:	:		
Db	172	SQWDEVIDLNLITGVFLCTQAAATKIMKKRKGKIINIASVVGIGIIGNIGOANYAARAKAGVIG	231	
Qy	235	FTKTVAEYASRNINVAIAPGFIASDMTAELEKKILSTIPLRGYQGPVEEVAGLVE	294	
	:	:		
	:	:		
	:	:		
	:	:		
	:	:		
Db	232	FSKTAAREGASRNINNVVCPGFITASDMTAKLGEDMEKKILGTIPLRGYQGPEDVAGLVE	291	
Qy	295	FLALNPAASYMTGQVLITIDGNVM	318	
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	:	:		
	:	:		
	:	:		
	:	:		
Db	292	FLALSPAASYTTGQAFITDGGIAI	315	

RESULT 2
 US-08-793-035-10
 ; Sequence 10, Application US/08793035
 ; Patent No. 6011201
 ; GENERAL INFORMATION:
 ; APPLICANT: Slabas, Antoni R.
 ; APPLICANT: White, Andrew
 ; APPLICANT: Chase, Dianne
 ; APPLICANT: Elborough, Keiran
 ; APPLICANT: Pentem, Phillip A.
 ; TITLE OF INVENTION: B-Ketocacyl ACP Reductase Genes From
 ; TITLE OF INVENTION: Brassica Napus
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: US
 ; ZIP: 77210-4433
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/793,035
 ; FILING DATE: 28-JUL-1997
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9414622.2
 ; FILING DATE: 20-JUL-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB95/01678
 ; FILING DATE: 17-JUL-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kammerer, Patricia A.
 ; REGISTRATION NUMBER: 29,775
 ; REFERENCE/DOCKET NUMBER: MOBT:132
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713.787.1400
 ; TELEFAX: 713.787.1440
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 315 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

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US-08-793-035-10

Query Match          70.1%; Score 1093; DB 3; Length 315;
Best Local Similarity 80.7%; Pred. No. 1.6e-101;
Matches 213; Conservative 28; Mismatches 23; Indels 0; Gaps 0;

Qy 55 VOTHVAAEQAVVKDATKLEAPVVVVVTGASRGIGKATALAGKAGCKVLVNYARSKEAE 114
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Db 52 VKAQATAVEQSTGEAEVKEVSPVVVVVTGASRGIGKATALSIGKAGCKVLVNYARSKEAE 111

Qy 115 EVSKEIEBASGGEALTFFGGDVSKADVEBSMKKALDKWGTTDVLVNNAGITRDTLLMRMK 174
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Db 112 EVSKQIEBAYGGOALTFFGGDVSKADVEAMKMTAIDAWGTTDVLVNNAGITRDTLLIRMK 171

Qy 175 SQMDVLDLNLGTGVLCTQATKMMKKRKGKINTASVVGLTCNTVCOANYSAKAGVIG 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 SQMDEVLDLNLGTGVLCTQATKIMMKRKRGRINTASVVGLTGNIGCOANYAAKAGVIG 231

Qy 235 FTKTVAREASRNINVNNAIAPGFIASDMTAELEBELEKKILSTIPLGRYQOPEVAGLVE 294
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 FSKTAAREGASRNINNVNVCFGFIASDMTAKLGEDMEKKILGTIPLGRYQOPEDVAGLVE 291

Qy 295 FLALNPAASYMTGGVLTFIDGGVMV 318

Db 292 FLALSPAASYITGOAFTIDGGIAI 315

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RESULT 3
US-09-238-481-2
; Sequence 2, Application US/09238481
; Patent No. 6110704
; GENERAL INFORMATION:
; APPLICANT: Huang, Jiansheng
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Rabg
; FILE REFERENCE: GM10192
; CURRENT APPLICATION NUMBER: US/09/238,481
; CURRENT FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-238-481-2

```

Query Match	42.2%	Score 658.5	DB 3	Length 246
Best Local Similarity	55.0%	Pred. No. 4.4e-58		
Matches 132	Conservative 44	Mismatches 63	Indels 1	Gaps 1
Qy	79	VVTGASRGIGKATALALGKAGCKVLVNYASRSKEAEVSEIKIASGGEALTFGGDVSKEA	138	
Db	8	LVTGASRGIGSIALQLAESGVNVAVNYAGSKKAEAVVEIKAKGVDSFALQANVADAD	67	
Qy	139	DVRSNMKAALDKNGTIDVLVNNAGITRDTLLMRKKSQWODVIDLNLVTQVFLCTQAAKTV	198	
Db	68	EVKAMIEKVYSQGSGLDVLVNNAGITRDNLLMRKKEQEWDDVDITNLKGVFNCTIQKATPQ	127	
Qy	199	MMKKRKKIKINIASVGLGTGVGQANYSAAKAGVIGFTKTVAREYASRNINNVAILAPGFI	258	
Db	128	MLQRSGAILNLSVVGAVGPNQANVATKAGVIGLTKSARELASRGITVNAVAPGFI	187	
Qy	259	ASDMTAEGBELBKILSTTILGRYGQPEEAVAGLVEFLALNPAAYSYMTGQVLTIDGGNVM	318	
Db	188	VSDMTALSDELKEOMLTQIPLARFGODTDIANTVAFIA-SDKAKYITGOTIHVNGWYMW	246	

RESULT 4
US-09-572-810A-2
; Sequence 2, Application US/09572810A
; Patent No. 6365387
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong

```

QY 259 ASDMTAELBELEKKILSTIPLGRYQPEVAGIYVFLALNPAASVMTGQVLIDGNVM 318
Db 191 VSDMTNALSDDLKQMLLEQIPLKRFGBEDTIDANTVAFIA--SDKAKYITGQTIHVNGGMYM 249

RESULT 6
US-09-239-052-2
; Sequence 2, Application US/09239052
; Patent No. 6346395
; GENERAL INFORMATION:
; APPLICANT: Holmes, David J.
; APPLICANT: Zhong, YiYi
; APPLICANT: Debouck, Christine
; APPLICANT: Jaworski, Deborah D.
; APPLICANT: Wang, Min
; APPLICANT: Warren, Richard L.
; APPLICANT: Kosmatka, Anna L.
; APPLICANT: McDevitt, Damien
; APPLICANT: Ingraham, Karen A.
; APPLICANT: Chalker, Alison F.
; APPLICANT: So, Chi Young
; APPLICANT: Wallis, Nicola G.
; APPLICANT: Pearson, Stewart C.
; TITLE OF INVENTION: FabG
; FILE REFERENCE: GM10191
; CURRENT APPLICATION NUMBER: US/09/239,052
; CURRENT FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-239-052-2

Query Match 38.3%; Score 597.5; DB 4; Length 243;
Best Local Similarity 50.6%; Pred. No. 5.8e-52;
Matches 126; Conservative 48; Mismatches 66; Indels 9; Gaps 3;

QY 72 KLEAPVVVTGASRGIGKATAIGALGKAGCKVLVNYARSKEA--EEVSKEIEASGGEAIT 129
Db 2 KLEHKNIFTGSSRGIGLAIAHKFAQAGANIVLN---SRGAISELLAEFSNVGIKVP 57

QY 130 FGDVSEKADVESMTKAAIDKWTIDVLYNNAGITDITLLMRKKSQWQDVIDLNTGVF 189
Db 58 ISGVDSDFAKRMIDQAIAGLSVDVLYNNAGITDITLLMRKKSQWQDVIDLNTGVF 117

QY 190 LCTQAATKVMKKRKKKINIASVWGLTGNVGQANYSAKAGVIGFTKTVAREVASRNIN 249
Db 118 NMTQSVLKPWKARQAGIINMSSVUGLMGNICQANYAASKAGLIGFTKSAREVASRNIR 177

QY 250 VNIAAGFTASDMTAELEBELEKKILSTIPLGRYQPEVAGIYVFLALNPAASVMTGQV 309
Db 178 VNVIAFGMIESDMTALISDKIKEATLAQIPMKFEQGAQVADITVFLA---GQDYLTVGV 234

QY 310 LTIDGGWVM 318
Db 235 IADGGLSM 243

RESULT 7
US-09-107-532A-4950
; Sequence 4950, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynx A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; STREET: 100 Beaver Street

```


GENERAL INFORMATION:

APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
 TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
 TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski L.L.P.
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,993

FILING DATE: September 26, 1997

CLASSIFICATION: 530

Prior APPLICATION DATA:

APPLICATION NUMBER: 08/729,594

FILING DATE: 11-October-1996

Prior APPLICATION DATA:

APPLICATION NUMBER: 08/562,114

FILING DATE: 22-No. 6399344ember-1995

Prior APPLICATION DATA:

APPLICATION NUMBER: 08/375,962

FILING DATE: 20-January-1995

Prior APPLICATION DATA:

APPLICATION NUMBER: 08/258,418

FILING DATE: 10-June-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6399344man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5517

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase

NAME/KEY:

US-08-937-993-13

Query Match 36.8%; Score 573.5; DB 4; Length 244;

Best Local Similarity 49.4%; Pred. No. 1.5e-49;

Matches 121; Conservative 45; Mismatches 74; Indels 5; Gaps 3;

QY 74 EAPVVVTGASRGIGKATLALGKAGCKVLVNYARSSKEAEVSKIEASGGEAITFGGD 133

DB 4 EGKIALVTGASRGIGRAIAETLAARGKV-IGTATSENGAQAI SDYLGA NGKGLML--N 59

QY 134 VSKEADVESNMKKAALDKWGTIDVLVNNAGITRDITLLMRMKSQWQDVIDLNTGVFLCTQ 193

DB 60 VTDPAESLVLEKTRAEFGEVDILVNNAGITRDITLLMRMKSQWQDVIDLNTGVFLCTQ 193

QY 194 AATKVMKKRKGKIIINTASVVLGTVNGVQANYSAAGVIGFTKTIVAREYASRNINVAI 253

DB 120 AVMEAMKKRGRITIGSVVGTGNGVQANYSAAGVIGFTKTIVAREYASRNINVAI 179

QY 254 APGTIASDMTAELEKILSTIPLGRYQGPVEVAGLVFELALNPAASVMTGOVLTD 313

DB 180 APGTIETDMTRALSDQDQAGILAVPAGRLGGAGQEIANAFAFLASDEAA-YIIGETILHVN 238

QY 314 GGMVM 318

DB 239 GGMVM 243

RESULT 12

US-09-252-991A-18645

; Sequence 18645; Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 18645

; LENGTH: 362

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

; US-09-252-991A-18645

Query Match 36.2%; Score 565.5; DB 4; Length 362;

Best Local Similarity 42.6%; Pred. No. 1.7e-48;

Matches 130; Conservative 54; Mismatches 108; Indels 13; Gaps 3;

QY 14 SSPAARGAAGAAAARRRGFTVFGGAARPSPTLRSGRGFGVQTHVAAVQAVVKDATKL 73

DB 70 SAGRAASWQASTGAARASIPMAWMAGRSPPRAP-----PWPBREGKGNPMSL 118

QY 74 EAPVVVTGASRGIGKATLALGKAGCKVLVNYARSSKEAEVSKIEASGGEAITFGGD 133

DB 119 QGKVALVTGASRGIGTQAIALLELGLGA-VVIGTATSASGAETKATLKVANGVEGAGLVLD 177

QY 134 VSKEADVESNMKKAALDKWGTIDVLVNNAGITRDITLLMRMKSQWQDVIDLNTGVFLCTQ 193

DB 178 VSSDESVAATLEHIQOHLGQPLIVVNNAGITRDITLLMRMKSQWQDVIDLNTGVFLCTQ 237

QY 194 AATKVMKKRKGKIIINTASVVLGTVNGVQANYSAAGVIGFTKTIVAREYASRNINVAI 253

DB 238 AVLRGMTKARWGLIINGSVVGAGNAGQTNVYAAKAGLEGFTALAREVGSRAITVNAV 297

QY 254 APGTIASDMTAELEKILSTIPLGRYQGPVEVAGLVFELALNPAASVMTGOVLTD 313

DB 298 APGTIETDMTRALSDQDQAGILAVPAGRLGGAGQEIANAFAFLASDEAA-YIIGETILHVN 356

QY 314 GGMVM 318

DB 357 GGMVM 361

RESULT 13

US-09-198-452A-309

; Sequence 309; Application US/09198452A

; Patent No. 655294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 309

; LENGTH: 251

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

; US-09-198-452A-309

Query Match

33.8%; Score 528; DB 4; Length 251;

Best Local Similarity 46.4%; Pred. No. 5.7e-45;
Matches 111; Conservative 41; Mismatches 85; Indels 2; Gaps 2;
QY 78 VVVTGASRGIGKATALGKAGCKVLYNVARSSKEAEVSKIEBASGEAITFGDVSKE 137
Db 13 VIVTGGSRGIGLIGIVKLFLENGADVEI-WGLNEERGQAVIESLTGLGGEVSFARVDVSHN 71
QY 138 ADVESMMKAALDKWGTIDVLNNAGITDITLLMRMKSQWQDVIDLNLTVFLCTQATK 197
Db 72 GGVKDCQVKFKDKNKIDILVNNAGITDITLLMRMSEDDWQSVISTNLTSYITCSSLVIR 131
QY 198 VMKRRKGKIINIASVVLGTGNVGQANYSAKAGVIGTKTVAREYASRNINVAIAPGF 257
Db 132 HMIKARSGIINVASIVAKIGSAGQTNVAAKAGIIATFKSLAKEVAARNIRVNCIAPGF 191
QY 258 IASDTMTELGELEKILSTIPLGRYQPEVAGLVEFLALNPAASYMTQVLTIDGM 316
Db 192 IETDMSVINDLKAELKSLIPLGRAGTPEDVARVALFLA-SQLSSYMTAQTLVVDGGL 249
RESULT 14
US-09-328-352-4761
; Sequence 4761, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03FA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4761
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4761

Query Match 31.1%; Score 484.5; DB 4; Length 262;
Best Local Similarity 42.9%; Pred. No. 1.4e-40;
Matches 108; Conservative 51; Mismatches 86; Indels 7; Gaps 4;
QY 68 KDATKLEAPVVVTGASRGIGKATALGKAGCKVLYNVARSSKEAEVSKIEI-EASGGE 126
Db 16 KNCMTQERKVALVTGASRGIGAAIAQQLIQGYFV-VGTATSESGAQLDTSFGQAGL 74
QY 127 AITFGGVSKEADVESMMKAALDKWGTIDVLNNAGITDITLLMRMKSQWQDVIDLNL 186
Db 75 AL-----DVRNLDETEAVVSHIEQYGPVLVNNAGITKDNLLRMSDEDDWDDILNIHLK 130
QY 187 GVFLCTQATKVMKRRKGKIINIASVVLGTGNVGQANYSAKAGVIGTKTVAREYASR 246
Db 131 AVTLRSRVUKMTKARFGRILINSSVVAHFANPGQANYSAKAGIBAFERSLAKENGSR 190
QY 247 NINVNIAIAPGFASDTMTELGELEKILSTIPLGRYQPEVAGLVEFLALNPAASYMT 306
Db 191 QITVNSVAPGFATMTDALSIEDIKMSQVALNRLGEPQDIANAVFLA-SDKAGIIT 249
QY 307 GOVLTIDGMM 318
Db 250 GTVLHVNGGLYM 261

RESULT 15
US-08-178-257-19
; Sequence 19, Application US/08178257
; Patent No. 6515205
; GENERAL INFORMATION:
; APPLICANT: LIEBERGSELL, MATTHIAS
; APPLICANT: STEINBUCHER, ALEXANDER
; TITLE OF INVENTION: PRODUCTION OF POLYALKANOATE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN, DABBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178.257
FILING DATE: 11-JAN-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01291
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9115245.4
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 9320/206058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEFAX: 202/822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Zoogloea ramigera
US-08-178-257-19

Query Match 30.7%; Score 479.5; DB 4; Length 241;
Best Local Similarity 45.2%; Pred. No. 3.9e-40;
Matches 109; Conservative 47; Mismatches 76; Indels 9; Gaps 6;
QY 77 VVVTGASRGIGKATALGKAGCKVLYNVARSSKEAEVSKIEBASGEAITFGDVSKE 136
Db 4 VALVTGSRGIGAAISIALKAAGYKVAASYAGN-----DAAKPKAETGIIV-YKMDVSS 58
QY 137 -EADVESMMKAALDKWGTIDVLNNAGITDITLLMRMKSQWQDVIDLNLTVFLCTQAA 195
Db 59 YEACVGEIAKVEAD-LGPIDVLNNAGITKDMFHKMTDPMNAVINTLGLFNMTHPV 117
QY 196 TKVMKRRKGKIINIASVVLGTGNVGQANYSAKAGVIGTKTVAREYASRNINVAIAP 255
Db 118 WSGMRDRSFGRIVNISSINGKQGMQGMQANYSAKAGDLGFTKALAQEAGKAGITVAICP 177
QY 256 GFTASDMTELGELEKILSTIPLGRYQPEVAGLVEFLALNPAASYMTQVLTIDG 314
Db 178 GYIGTEMVRAIPEKVLNERIIPQIPVGLRGEPEIARIIVVFLA-SDEAGFITGSTISANG 236
QY 315 G 315
Db 237 G 237

Search completed: November 7, 2003, 21:05:29
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 21:04:32 ; Search time 49 Seconds
(without alignments)
1114.618 Million cell updates/sec

Title: US-10-024-806-2

Perfect score: 1560

Sequence: 1 MATAAATAAAAVSSPAARG.....NPRAASYMTGQVLIDGGMV 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*

17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1560	100.0	318	12	US-10-024-806-2
2	1279	82.0	312	12	US-10-024-806-4
3	1128	72.3	320	12	US-10-024-806-6
4	986.5	63.2	299	12	US-10-024-806-8
5	658.5	42.2	246	9	US-09-815-242-5461
6	658.5	42.2	246	9	US-09-815-242-12123
7	658.5	42.2	246	9	US-09-815-242-12803
8	658.5	42.2	246	9	US-09-815-242-13100
9	598.5	38.4	245	9	US-09-815-242-10921
10	597.5	38.3	243	9	US-09-815-242-13360
11	597.5	38.3	243	9	US-09-815-242-13561
12	576.5	37.0	244	9	US-09-815-242-10126
13	573.5	36.8	244	11	US-09-849-092-13
14	556	35.6	247	9	US-09-815-242-11893
15	545.5	35.0	242	9	US-09-815-242-10974

16	529	33.9	247	10	US-09-479-040-9	Sequence 9, Appl
17	528	33.8	239	15	US-10-156-761-13989	Sequence 13989, A
18	496.5	31.8	247	9	US-09-815-242-11342	Sequence 11342, A
19	486.5	31.2	247	9	US-09-815-242-11514	Sequence 11514, A
20	478.5	30.7	313	15	US-10-156-761-11190	Sequence 11190, A
21	467.5	30.0	158	12	US-10-288-930-85	Sequence 85, Appl
22	459	29.4	237	9	US-09-823-901-2	Sequence 2, Appl
23	459	29.4	237	15	US-10-175-696-14	Sequence 14, Appl
24	458	29.4	253	15	US-10-156-761-14536	Sequence 14536, A
25	451	28.9	240	12	US-10-166-225A-179	Sequence 179, App
26	451	28.9	261	10	US-09-940-037A-29	Sequence 29, Appl
27	450	28.8	226	10	US-09-895-913A-362	Sequence 362, App
28	448.5	28.7	253	9	US-09-815-242-10279	Sequence 10279, A
29	447	28.7	261	12	US-10-004-115A-36	Sequence 36, Appl
30	447	28.7	261	12	US-10-327-108-12	Sequence 12, Appl
31	444.5	28.5	261	15	US-10-187-267A-33	Sequence 33, Appl
32	441.5	28.3	253	9	US-09-815-242-13878	Sequence 13878, A
33	433.5	27.8	641	10	US-09-364-847-10	Sequence 10, Appl
34	433	27.8	642	10	US-09-364-847-59	Sequence 59, Appl
35	426.5	27.3	246	10	US-09-364-847-6	Sequence 6, Appl
36	426.5	27.3	641	10	US-09-364-847-19	Sequence 19, Appl
37	426.5	27.3	642	10	US-09-364-847-61	Sequence 61, Appl
38	424.5	27.2	243	12	US-10-238-075-837	Sequence 837, App
39	423.5	27.1	259	10	US-09-931-186-17	Sequence 17, Appl
40	417.5	26.8	906	14	US-10-060-230-19	Sequence 19, Appl
41	417.5	26.8	906	14	US-10-060-230-20	Sequence 20, Appl
42	411.5	26.4	315	15	US-10-156-761-13732	Sequence 13732, A
43	411.5	26.4	906	14	US-10-060-230-21	Sequence 21, Appl
44	411.5	26.4	906	14	US-10-060-230-22	Sequence 22, Appl
45	402	25.8	261	10	US-09-971-536-74	Sequence 74, Appl

ALIGNMENTS

RESULT 1

US-10-024-806-2

; Sequence 2, Application US/10024806

; Publication No. US20030167532A1

; GENERAL INFORMATION:

; APPLICANT: Zheng, Peizhong

; APPLICANT: Li, Chun Ping

; APPLICANT: Nichols, Scott E.

; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and

; TITLE OF INVENTION: Their use in PHA Production in Plants

; FILE REFERENCE: 35718/241887

; CURRENT APPLICATION NUMBER: US/10/024,806

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/258,417

; PRIOR FILING DATE: 2000-12-27

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 318

; TYPE: PRT

; ORGANISM: Zea mays

US-10-024-806-2

Query Match 100.0%; Score 1560; DB 12; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-130;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MATAAATAAAAVSSPAARGAAGAAASRRGVTFTGGGAARFPTLRSRGFGSGVTHVA	60
Db	1	MATAAATAAAAVSSPAARGAAGAAASRRGVTFTGGGAARFPTLRSRGFGSGVTHVA	60
QY	61	AVEQAVVKDATTLEAPVVVVVTGASRGIGKATALALGKAGCKVLNVARSKEAEVSKET	120
Db	61	AVEQAVVKDATTLEAPVVVVVTGASRGIGKATALALGKAGCKVLNVARSKEAEVSKET	120
QY	121	EASGGEATFTGGDVSKAEADVESMKAAALDKWTGTTDVLVNNAGTTRDTLLMRKKSQWDV	180
Db	121	EASGGEATFTGGDVSKAEADVESMKAAALDKWTGTTDVLVNNAGTTRDTLLMRKKSQWDV	180

Qy 181 IDLNLGTGVLCTQATKVMKKRKGKIINIASVVLGTGNGVQANYSAAGVIGFTKVA 240
Db 181 IDLNLGTGVLCTQATKVMKKRKGKIINIASVVLGTGNGVQANYSAAGVIGFTKVA 240
Qy 241 REYASRNINVAIAPGFTASDMTAELEKILSTIPLGRYQOPPEVAGLVEFLALNP 300
Db 241 REYASRNINVAIAPGFTASDMTAELEKILSTIPLGRYQOPPEVAGLVEFLALNP 300
Qy 301 AASYMTGQVLTIIDGGVM 318
Db 301 AASYMTGQVLTIIDGGVM 318

RESULT 2
US-10-024-806-4
; Sequence 4, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; FILE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/258,417
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Zea mays
US-10-024-806-4

Query Match 82.0%; Score 1279; DB 12; Length 312;
Best Local Similarity 82.0%; Pred. No. 1.7e-105;
Matches 264; Conservative 20; Mismatches 20; Indels 18; Gaps 3;
Qy 4 AATAAATAAASVSPAAAGAAAGAAASRRGFVTFGGGAARFSPILRSRGFS-----GVQ 56
Db 2 AATAAATAAASVSPAAAGAAAGAAASRRGFVTFGGGAARFSPILRSRGFS-----GVQ 56
Qy 57 THVAAVEQAVVYKDATKLEAPVVVVTGASRGIGKATATGAGCKVLTGNGVQANYSAAGVIGFT 116
Db 51 THVTAVDQAVVYKDATKLEAPVVVVTGASRGIGKATATGAGCKVLTGNGVQANYSAAGVIGFT 110
Qy 117 SKETIEASGGEALTGGDVSKEADVESMMKALDKWGTIDVLVNNAGITRDITLLMRKSK 176
Db 111 SKETIEASGGEALTGGDVSKEADVESMMKALDKWGTIDVLVNNAGITRDITLLMRKSK 170
Qy 177 WQVDIDLNLGTGVLCTQATKVMKKRKGKIINIASVVLGTGNGVQANYSAAGVIGFT 236
Db 171 WQDAIDLNLGTGVLCTQATKVMKKRKGKIINIASVVLGTGNGVQANYSAAGVIGFT 230
Qy 237 KTAREYASRNINVAIAPGFIASDMTAELEKILSTIPLGRYQOPPEVAGLVEFL 296
Db 231 KTAREYASRNINVAIAPGFIASDMTAELEKILSTIPLGRYQOPPEVAGLVEFL 290
Qy 297 ALNPAASYMTGQVLTIIDGGVM 318
Db 291 ALNPAASYMTGQVLTIIDGGVM 312

RESULT 3
US-10-024-806-6
; Sequence 6, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping

; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; FILE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/258,417
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Glycine max
US-10-024-806-6

Query Match 72.3%; Score 1128; DB 12; Length 320;
Best Local Similarity 72.2%; Pred. No. 4.7e-92;
Matches 234; Conservative 29; Mismatches 43; Indels 18; Gaps 3;
Qy 8 AAAAASVSPAAAGAAAGAAASRRGFVTFGGGAARFSPILRSRGFS-----RSGRGF--SG 54
Db 2 ASIAGSNVARTANFAGSNRK-----IGQIRQWSPILNLRPVSGLRHSNTPFSSSG 56
Qy 55 VOTHAAVEQAVVYKDATKLEAPVVVVTGASRGIGKATATGAGCKVLTGNGVQANYSAAGVIGFT 114
Db 57 VRAQVATLEAGTCAKQVEAPVVVVTGASRGIGKATATGAGCKVLTGNGVQANYSAAGVIGFT 116
Qy 115 EVSKEIEASGGEALTGGDVSKEADVESMMKALDKWGTIDVLVNNAGITRDITLLMRKSK 174
Db 117 EVSKEIEASGGEALTGGDVSKEADVESMMKALDKWGTIDVLVNNAGITRDITLLMRKSK 176
Qy 175 SQWQVDIDLNLGTGVLCTQATKVMKKRKGKIINIASVVLGTGNGVQANYSAAGVIGFT 234
Db 177 SQWQVDIDLNLGTGVLCTQATKVMKKRKGKIINIASVVLGTGNGVQANYSAAGVIGFT 236
Qy 235 FTKTAREYASRNINVAIAPGFIASDMTAELEKILSTIPLGRYQOPPEVAGLVE 294
Db 237 LTKTAREYASRNINVAIAPGFIASDMTAELEKILSTIPLGRYQOPPEVAGLVE 296
Qy 295 FLALNPAASYMTGQVLTIIDGGVM 318
Db 297 FLALNPAASYMTGQVLTIIDGGVM 320

RESULT 4
US-10-024-806-8
; Sequence 8, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; FILE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/258,417
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Glycine max
US-10-024-806-8

Query Match 63.2%; Score 986.5; DB 12; Length 299;
Best Local Similarity 71.2%; Pred. No. 1.6e-79;
Matches 205; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
Qy 32 FVTFGGGAARFSPILRSRGFSGVQTHAAVEQAVVYKDATK-LEAPVVVVTGASRGIGK 90

Db 12 FRTKGPARKVPSQVLAFORSNSNGSPSPSEQLLEASQKNWEAPVVVTGASRGIGRA 71
QY 91 TALALGAGCKVLVNYARSSKEAEVSEKTEASGGEAITFGGDIVSKADVSEMMKAALDK 150
Db 72 IALSLGAPCKVLVNYARSSQAEVSNLIEAFGGQALTPEGDVSEADVESMIRTAEDA 131
QY 151 WGTIDVLNNAGITRDITLLMRKKSQMDVIDNLNLTGVFLCTQAAATKVMKKKGGKIINI 210
Db 132 WGTIDVLNNAGITRDITLLMRKKSQMDVIDNLNLTGVFLCTQAAATKVMKKKGGKIINI 191
QY 211 ASVVGLTGNVQOANYSAAGVIGFTKTVAEYASRNINVNALAPGFIASDMTAEIAGEEL 270
Db 192 TSVIGQVGNVQOANYSAAGVIGFTKTVAEYASRNINVNALAPGFIASDMTANLAPGI 251
QY 271 EKKILSTIPIGRGQPEEAGLVFLALNPAASVMTQVLTIDGGMVM 318
Db 252 EKKRLEIPIGRIGQPEEAGLVFLALNPAASVMTQVLTIDGGLAM 299

RESULT 5

US-09-815-242-5461
; Sequence 5461, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5461
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5461

Query Match 42.2%; Score 658.5; DB 9; Length 246;
Best Local Similarity 55.0%; Pred. No. 1.6e-50;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;
QY 79 VVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSEKTEASGGEAITFGGDIVSKEA 138
Db 8 LVTGASRGIGRSIALQAEAGVNVAVNYAGSKEAEVSEKTEASGGEAITFGGDIVSKEA 67
QY 139 DYESMMKAALDKWGTIDVLNNAGITRDITLLMRKKSQMDVIDNLNLTGVFLCTQAAATK 198
Db 68 EVKAMIKVVSQFSGSLDVLNNAGITRDITLLMRKKEQWDDVIDITNLKGVFNFCIQKATPQ 127
QY 199 MMKRRGKIINIASVVGLTGNVQOANYSAAGVIGFTKTVAEYASRNINVNALAPGFI 258

RESULT 7

US-09-815-242-12803
; Sequence 12803, Application US/09815242
; Patent No. US20020061569A1

Db 128 MURQSGALINSSVVGAVNPGQANYATKAGVIGFTKSAARELASRGITVNAVAPGI 187
QY 259 ASDMTAEIAGEEKKILSTIPIGRGQPEEAGLVFLALNPAASVMTQVLTIDGGMVM 318
Db 188 VSDMTDALSDELKEQMLTQIPLARFGQDITANTVAFLA-SDKAKYITGQTHVNGGMVM 246

RESULT 6

US-09-815-242-12123
; Sequence 12123, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12123
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12123

Query Match 42.2%; Score 658.5; DB 9; Length 246;
Best Local Similarity 55.0%; Pred. No. 1.6e-50;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;
QY 79 VVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSEKTEASGGEAITFGGDIVSKEA 138
Db 8 LVTGASRGIGRSIALQAEAGVNVAVNYAGSKEAEVSEKTEASGGEAITFGGDIVSKEA 67
QY 139 DYESMMKAALDKWGTIDVLNNAGITRDITLLMRKKSQMDVIDNLNLTGVFLCTQAAATK 198
Db 68 EVKAMIKVVSQFSGSLDVLNNAGITRDITLLMRKKEQWDDVIDITNLKGVFNFCIQKATPQ 127
QY 199 MMKRRGKIINIASVVGLTGNVQOANYSAAGVIGFTKTVAEYASRNINVNALAPGFI 258
Db 128 MURQSGALINSSVVGAVNPGQANYATKAGVIGFTKSAARELASRGITVNAVAPGI 187
QY 259 ASDMTAEIAGEEKKILSTIPIGRGQPEEAGLVFLALNPAASVMTQVLTIDGGMVM 318
Db 188 VSDMTDALSDELKEQMLTQIPLARFGQDITANTVAFLA-SDKAKYITGQTHVNGGMVM 246

```

; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12803
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12803

Query Match 42.2%; Score 658.5; DB 9; Length 246;
Best Local Similarity 55.0%; Pred. No. 1.6e-50;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;

QY 79 VVTGASRGIGKATALAGKAGCKLVNVARSSKEAEVSKIEASGGEALTFFGDDYSKEA 138
Db 8 LVTGASRGIGKRSIALQAEAGYNVAVNAGSKEAEVVEIKAKGVDSFAIQANVADAD 67

QY 139 DVESMMKAALDKWGTIDVLNNAGITRDTLLMRMKSQWODVIDLNLTVFLCTQATKV 198
Db 68 EVKAMIKVVSQFSGSLDVLNNAGITRDNLLMRMKEQWDDVIDTDLNKGVCIOKATPQ 127

QY 199 MMKRGKGIINIASVUGLTGNVGOANYSAKAGVIGFTKTVAEYASRNINVAIAPGFI 258
Db 128 MLQSRGAIINLSSVVGAVGNPGQANYVATKAGVIGLTKSAARELASRGITVNAVAPGFI 187

QY 259 ASDMTAELGEEKKILSTPLGRYGQPEVAGLVEFLALNPAASVMTGQVLTDGGMVM 318
Db 188 VSDMTDALSDELKEQMLTQIPARFGQDTDIANTVAFIA-SDKAKYITGQTIHVNGGMVM 246

RESULT 8
US-09-815-242-13100
; Sequence 13100, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; FILE REFERENCE: ELITRA.011A

Query Match 42.2%; Score 658.5; DB 9; Length 246;
Best Local Similarity 55.0%; Pred. No. 1.6e-50;
Matches 132; Conservative 44; Mismatches 63; Indels 1; Gaps 1;

QY 79 VVTGASRGIGKATALAGKAGCKLVNVARSSKEAEVSKIEASGGEALTFFGDDYSKEA 138
Db 8 LVTGASRGIGKRSIALQAEAGYNVAVNAGSKEAEVVEIKAKGVDSFAIQANVADAD 67

QY 139 DVESMMKAALDKWGTIDVLNNAGITRDTLLMRMKSQWODVIDLNLTVFLCTQATKV 198
Db 68 EVKAMIKVVSQFSGSLDVLNNAGITRDNLLMRMKEQWDDVIDTDLNKGVCIOKATPQ 127

QY 199 MMKRGKGIINIASVUGLTGNVGOANYSAKAGVIGFTKTVAEYASRNINVAIAPGFI 258
Db 128 MLQSRGAIINLSSVVGAVGNPGQANYVATKAGVIGLTKSAARELASRGITVNAVAPGFI 187

QY 259 ASDMTAELGEEKKILSTPLGRYGQPEVAGLVEFLALNPAASVMTGQVLTDGGMVM 318
Db 188 VSDMTDALSDELKEQMLTQIPARFGQDTDIANTVAFIA-SDKAKYITGQTIHVNGGMVM 246

RESULT 9
US-09-815-242-10921
; Sequence 10921, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; FILE REFERENCE: ELITRA.011A
```

```
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10921
/ LENGTH: 245
/ TYPE: PRT
/ ORGANISM: Enterococcus faecalis
US-09-815-242-10921

Query Match      38.4%; Score 598.5; DB 9; Length 245;
Best Local Similarity 52.3%; Pred. No. 3.5e-45;
Matches 126; Conservative 42; Mismatches 68; Indels 5; Gaps 2;

QY 78 VVVTGSRGIGKATATAGAGCKVLVNARSKEAEVSKTEASGGRAITPGGDSKE 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 VFTGSTRGIGKAVAFKAGANIVLN--GRSEITPEQOEIAFGVKICGLSGDISDF 65

QY 138 ADVESMMKAALDKWGTIDVLNNAGITRDITLLMRMKSQWQDVIDLNLGTVLCTQAATK 197
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 DAAGEMIQTAVDQGSIDILVNNAGITNDKLLRMTKEDFNACDILNLGTFNMTQAAVK 125

QY 198 VMKXKRGKIINIATSVVGLTGNVGOANYSAAGVIGFTKTVAEYASRNINVAIAPGF 257
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 RMKQSSGRIINWASVSLMGVGOANYAASKAGVGVGFTKSVAREVAPRGITCNALAPGF 185

QY 258 IASDWTAEELGEEKILSTIPLGRYGOPEVAGIVEFLALNPAASVMTGQVLTIDGGMV 317
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 IQTMDTVLSEKVKTKQNAQIPLQTEQVEDVAATAIFLAKSP---YITGQVNVVDGLV 242

QY 318 M 318
Db 243 M 243

RESULT 10
US-09-815-242-13360
/ Sequence 13360, Application US/09815242
/ Patent No. US20020061569A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13360
/ LENGTH: 243
/ TYPE: PRT
/ ORGANISM: Streptococcus pneumoniae
US-09-815-242-13581

Query Match      38.3%; Score 597.5; DB 9; Length 243;
Best Local Similarity 50.6%; Pred. No. 4.3e-45;
Matches 126; Conservative 48; Mismatches 66; Indels 9; Gaps 3;

/ TYPE: PRT
/ ORGANISM: Streptococcus pneumoniae
US-09-815-242-13360

Query Match      38.3%; Score 597.5; DB 9; Length 243;
Best Local Similarity 50.6%; Pred. No. 4.3e-45;
Matches 126; Conservative 48; Mismatches 66; Indels 9; Gaps 3;
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Search completed: November 7, 2003, 21:09:56
Job time : 50 secs

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OM protein - protein search, using sw model

Run on: November 7, 2003, 20:54:56 ; Search time 26 Seconds
(without alignments)
1176.217 Million cell updates/sec

Title: US-10-024-806-2
Perfect score: 1560
Sequence: 1 MATAAATAAAVSSPAARG.....NPAASYMTGQVLIDGWMW 318

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616882 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76.*

1: Piri.*

2: Piri.*

3: Piri.*

4: Piri.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1130	72.4	320	2 S22450	3-oxoacyl-[acyl]-ca
2	1030.5	66.1	319	2 S22416	3-oxoacyl-[acyl]-ca
3	984	63.1	308	2 A86378	protein F21J9.2 [i
4	832	53.3	270	2 T00667	3-oxoacyl-[acyl]-ca
5	800.5	51.3	247	2 S77280	3-oxoacyl-[acyl]-ca
6	794.5	50.9	251	2 AH2042	3-oxoacyl-[acyl]-ca
7	712.5	45.7	246	2 C83961	3-oxoacyl-[acyl]-ca
8	711.5	45.6	246	2 A69621	3-oxoacyl-[acyl]-ca
9	686.5	44.0	247	2 AG1300	3-ketoacyl-acyl ca
10	681.5	43.7	247	2 AG1672	3-ketoacyl-acyl ca
11	669.5	42.9	249	2 F97338	3-ketoacyl-acyl ca
12	658.5	42.2	246	2 B89896	3-oxoacyl-[acyl]-ca
13	639.5	41.0	254	2 G75333	3-oxoacyl-[acyl] car
14	621.5	39.8	248	2 F82128	3-oxoacyl-[acyl]-ca
15	612.5	39.3	243	2 E97919	hypothetical prote
16	597.5	38.3	243	2 G95048	3-oxoacyl-[acyl]-ca
17	596.5	38.2	243	2 G72219	3-oxoacyl-[acyl]-ca
18	592	37.9	244	2 T12051	3-oxoacyl-[acyl]-ca
19	584.5	37.5	244	2 H22417	3-oxoacyl-[acyl]-ca
20	584	37.4	139	2 S22417	3-oxoacyl-[acyl]-ca
21	576.5	37.0	244	1 B42147	3-oxoacyl-[acyl]-ca
22	575.5	36.9	248	2 H70447	3-oxoacyl-[acyl]-ca
23	574.5	36.8	244	2 AD0642	3-oxoacyl-[acyl]-ca
24	573.5	36.8	244	2 G90812	3-oxoacyl-[acyl]-ca
25	573.5	36.8	244	2 C85672	3-oxoacyl-[acyl]-ca
26	571	36.6	247	2 F82776	3-oxoacyl-[acyl]-ca
27	559	35.8	248	2 F81971	probable 3-oxoacyl
28	559	35.8	248	2 E81026	3-oxoacyl-[acyl]-ca
29	558.5	35.8	244	2 AB0195	3-oxoacyl-[acyl]-ca

30	556	35.6	247	2 T12020	3-oxoacyl-[acyl]-ca
31	545.5	35.0	242	2 D64051	3-oxoacyl-[acyl]-ca
32	545.5	35.0	247	2 A81388	3-oxoacyl-[acyl]-ca
33	542.5	34.8	248	2 E81695	3-oxoacyl-[acyl]-ca
34	537.5	34.5	244	2 T44434	3-oxoacyl-[acyl]-ca
35	532.5	34.1	248	2 F71538	probable oxoacyl (
36	531	34.0	246	2 H84136	3-oxoacyl-[acyl]-ca
37	528	33.8	248	2 H85527	oxoacyl (carrier p
38	528	33.8	248	2 D72096	3-oxoacyl-[acyl]-ca
39	523.5	33.6	245	2 AG3436	short-chain dehydr
40	516.5	33.1	234	2 T36779	probable 3-oxoacyl-
41	508.5	32.6	241	2 F71636	3-oxoacyl reductas
42	508	32.6	246	2 A87457	3-oxoacyl-[acyl]-ca
43	507.5	32.5	245	2 AF2711	3-oxoacyl-[acyl]-ca
44	507.5	32.5	245	2 D97493	3-oxoacyl-[acyl]-ca
45	496.5	31.8	247	1 A64590	probable 3-oxoacyl

ALIGNMENTS

RESULT 1

S22450
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor, NADPH-dependent [N; Alternate names: beta-ketoacyl-ACP reductase
C; Species: Cuphea lanceolata
C; Date: 16-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 17-Mar-2000
C; Accession: S22450; S19832
R; Klein, B.; Pawlowski, K.; Hoerickx-Grandpierre, C.; Schell, J.; Toepfer, R.
Mol. Gen. Genet. 233, 122-128, 1992
A; Title: Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta-ketoacyl-ACP reductase
A; Reference number: S22450; MUID:92293104; PMID:1376402
A; Accession: S22450
A; Molecule type: mRNA
A; Residues: 1-320 <KLE>
A; Cross-references: EMBL:X64566; NID:g18045; PIDN:CAA45866.1; PID:g18046
A; Experimental source: immature embryo
C; Genetics:
A; Gene: Clkr27
A; Genome: nuclear
C; Function:
A; Description: EC 1.1.1.100 [validated, MUID:92293104]
A; Pathway: fatty acid biosynthesis
A; Note: Integral part of the fatty acid synthase type II
C; Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C; Keywords: chloroplast; fatty acid biosynthesis; NADP; oxidoreductase
F; 1-63/Domain: transit peptide (chloroplast) #status predicted <TNP>
F; 64-320/Product: 3-oxoacyl-[acyl-carrier-protein] reductase #status predicted <MAT>
F; 78-258/Domain: short-chain alcohol dehydrogenase homology <SADH>
F; 227/Active site: Tyr #status predicted

Query Match 72.4%; Score 1130; DB 2; Length 320;

Best Local Similarity 69.0%; Pred. No. 8.2e-68;

Matches 231; Conservative 31; Mismatches 41; Indels 32; Gaps 4;

QY 1 MATAAATAAAVSSPAARGAAGAAASRRGFTVFGGAARFSPPT 45

Db 1 MATAAAGCGAVALKSLGRLCTPQQLSPVLAG-----FGSHAASFPPI 46

QY 46 LBSGRGF--SGVQTHVAAYEAQAVKDATKLEAPVVVVTGASRGIGKATALAGKAGCKVL 103

Db 47 L-STRSIATSGTGRAQVATAEKVSAGAGQSVSPVIVTGAISRGIGKATIALSLGKAGCKVL 105

QY 104 VNYARSSKEAEVSKIEASGGEATFFGDDVSKEDVESMKAAALDKWGTIDVLVNNAGT 163

Db 106 VNYARSSKEAEVSKIEAFGGQALTFGGDVSKEDVEAMIKTAVDAWGTIDVLVNNAGI 165

QY 164 TRDTLLMRKKSQWDVIDLNLTVGLCTQAATKVMKKRKGKIINIASVWGLTGNVGA 223

Db 166 TRDGLLMRKKSQWDVIDLNLTVGLCTQAATKVMKKRKGKIINIASVWGLVGNVGA 225

QY 224 NYSAKAGVIGTKTVAREYASRNINVAIPGTIASDMTAEGLBELEKILSTIPLGRY 283

Db 224 NYSAKAGVIGTKTVAREYASRNINVAIPGTIASDMTAEGLBELEKILSTIPLGRY 283

Db 226 NYSAAKAGVIGTKTVAREYASRNINNVNAPGFTSSDWTSKLGGDINKKILETIPLGRY 285
 QY 284 GQPEVAGLVFELALNPASVMTGQVLITDGMVM 318
 Db 286 GQPEVAGLVFELALNPASSVMTGQVFTIDGMVM 320
 RESULT 2
 S22416
 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 11-Jun-1999
 C;Accession: S22416
 R;Slabas, A.R.; Chase, D.; Nishida, I.; Murata, N.; Sidebottom, C.; Safford, R.; Sheldon
 Biochem. J. 283: 321-326, 1992
 A;Title: Molecular cloning of higher-plant 3-oxoacyl-(acyl carrier protein) reductase. S
 A;Reference number: S22416; MUID:92246853; PMID:1575676
 A;Accession: S22416
 A;Molecule type: mRNA
 A;Residues: 1-319 <SLA>
 A;Cross-references: EMBL:X64464; NID:gl6204; PIDN:CAA45794.1; PID:gl6205
 A;Note: the authors translated the codon CTT for residue 33 as Ile, CGA for residue 44 a
 as Asn, CCC for residue 256 as Ala, AAA for residue 286 as Arg, and CCT for residue 301
 C;Genetics:
 A;Genome: nuclear
 C;Function:
 A;Pathway: fatty acid biosynthesis
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 F;1-59/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F;60-319/Product: 3-oxoacyl-(acyl-carrier-protein) reductase #status predicted <NAT>
 F;77-257/Domain: short-chain alcohol dehydrogenase homology <SADH>
 F;226/Active site: Tyr #status predicted
 Query Match 66.1%; Score 1030.5; DB 2; Length 319;
 Best Local Similarity 67.4%; Pred. No. 3.2e-61;
 Matches 215; Conservative 36; Mismatches 63; Indels 5; Gaps 4;
 QY 4 AAATAAAAVSSPAARGAAGAAASR-RGFTVFGGGAARFSP-TLRSRGFSG--VQTHV 59
 Db 2 AAATAAPRLISLKV-GKLGFREISQIQQLAPLHSAIPHFGMLRCRSPFSTSVVQAQA 60
 QY 60 AAQVAVKQATKLEAPVNVVTGASRGIGKATATLALGKAGCKVLNVNARSKEAEYSKE 119
 Db 61 TATEQSPGVQVQVSPVVTGASRGIGKATATLALGKAGCKVLNVNARSKEAEYAKQ 120
 QY 120 IEASGGBAITPGDVSKEADVSMKKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQD 179
 Db 121 IEYGGQAITPGDVSKEATDVDMKMTALDKWGTIDVLVNNAGITRDTLLMRKKSQWDE 180
 QY 180 VIDNLGTVFLCTCAATKVMKKKGIINIASVVLGTGNVGOANYAAKAGVIGFTKTV 239
 Db 181 VIALNLGTVFLCTCAATKVMKKKGIINIASVVLGTGNVGOANYATATRGVVISFSETP 240
 QY 240 AREYASRNINNVNAPGFIASDMTAELEKEKILSTIPLGRYQGPVEVAGLVFELALN 299
 Db 241 AREGASRNINNVVCPGFIASDMTAELEGEKILSTIPLGRYKAEVAGLVFELALS 300
 QY 300 PAASVMTGQVLITDGMVM 318
 Db 301 PAASYITGQAFITDGGIAI 319

RESULT 3
 A86378
 protein F21J9.2 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 01-Mar-2002
 C;Accession: A86378
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: A86378
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <SFO>
 A;Cross-references: GB:AE005172; NID:g9743327; PIDN:AAF97951.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 63.1%; Score 984; DB 2; Length 308;
 Best Local Similarity 65.1%; Pred. No. 3.8e-58;
 Matches 207; Conservative 32; Mismatches 65; Indels 14; Gaps 3;
 QY 4 AAATAAAAVSSPAARGAAGAAASR-RGFTVFGGGAARFSP-TLRSRGFSG--VQTHV 60
 Db 2 AAATAAPRLISLKVAKLGFREISQIQQLAPLHSAIPHFGMLRCRSPFSTSVVQAQA 61
 QY 61 AVEQAVVQKATKLEAPVNVVTGASRGIGKATATLALGKAGCKVLNVNARSKEAEYSKEI 120
 Db 62 ATEQSPGVQVQVSPVVTGASRGIGKATATLALGKAGCKVLNVNARSKEAEYAKQI 121
 QY 121 EASGGBAITPGDVSKEADVSMKKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDV 180
 Db 122 EYGGQAITPGDVSKEATDVDMKMTALDKWGTIDVLVNNAGITRDTLLMRKKSQWDEV 181
 QY 181 IDNLGTVFLCTCAATKVMKKKGIINIASVVLGTGNVGOANYAAKAGVIGFTKTV 240
 Db 182 IALNLGTVFLCTQ-----GRILNLSVVLGTGNVGOANYAAKAGVIFSKTAA 230
 QY 241 REYASRNINNVNAPGFIASDMTAELEKEKILSTIPLGRYQGPVEVAGLVFELALNP 300
 Db 231 REGASRNINNVVCPGFIASDMTAELEGEKILSTIPLGRYKAEVAGLVFELALSP 290
 QY 301 AASVMTGQVLITDGMVM 318
 Db 291 AASYITGQAFITDGGIAI 308

RESULT 4
 T00667
 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) F316.30 - Arabidopsis thaliana
 N;Alternate names: beta-oxoacyl-(acyl carrier protein); protein F316.30
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 29-Oct-1999
 C;Accession: T00667
 R;Federspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Arau
 j; Vysockaia, V.S.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
 submitted to the EMBL Data Library, February 1998
 A;Reference number: Z14197
 A;Accession: T00667
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-270 <FED>
 A;Cross-references: EMBL:AC002396; NID:g2749918; PIDN:AA00590.1; PID:g28882; GSPDB:GN
 C;Genetics:
 A;Gene: ATPSF316.30
 A;Map position: 1
 A;Introns: 55/1; 102/3; 120/3; 147/3; 163/1; 194/3; 239/3
 A;Function: fatty acid biosynthesis
 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
 C;Keywords: fatty acid biosynthesis; NADP; oxidoreductase
 F;77-246/Domain: short-chain alcohol dehydrogenase homology <SADH>
 Query Match 53.3%; Score 832; DB 2; Length 270;

Best Local Similarity 63.6%; Pred. No. 3.9e-48;
Matches 178; Conservative 27; Mismatches 61; Indels 14; Gaps 3;

QY 4 AAATAAAVSSPAAGAAAGAAASRRGFTVFGGAARFSP-TLRSGRFGSG--VQTHVA 60
Db 2 AAATAAPRLISLKAVALKGFREISQIRQLAPLHSAIPHFGLMCRKSRPFSTSVVKAQAT 61

QY 61 AVQAVVKDATKLEAPVVVVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSEKI 120
Db 62 ATEQSPGEVQVQVSPVVVITGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSEKI 121

QY 121 EASGGEAITFGDVSKEADVESMMKAALDKWGTIDVLVNNAGITRDITLLMRKKSQWQDV 180
Db 122 EYGGQAITFGDVSKEADVESMMKAALDKWGTIDVLVNNAGITRDITLLMRKKSQWQDV 181

QY 181 IDNLTVGVLCTQATKVMKRGKIKINIASVVLGTVGVQVQVQVQVQVQVQVQVQV 240
Db 182 IALNLTGVFLCTQ-----GRIINISSVVLGTVGVQVQVQVQVQVQVQVQVQV 230

QY 241 REVASRNINVAIAPGFIASDMTAELEGELEKILSTIPL 280
Db 231 REGASRNINNVVCPGFIASDMTAELEGELEKILSTIPL 270

RESULT 5
S77280
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Synecocystis sp. (strain PC
N;Alternate names: protein sir0886
C;Species: Synecocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S77280
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, I.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
S.
A;Reference number: S77280; MUID:97061201; PMID:8905231
A;Accession: S77280
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-247 <KAN>
A;Cross-references: EMBL:D90907; GB:AB001339; NID:g1652618; PIDN:BAAL7614.1; PID:g165269
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: fabG
C;Function:
A;Pathway: fatty acid biosynthesis
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: fatty acid biosynthesis; NADP; oxidoreductase
P;7-187/Domain: short-chain alcohol dehydrogenase homology <SADH>
P;156/Active site: Tyr #status predicted

Query Match 51.3%; Score 800.5; DB 2; Length 247;
Best Local Similarity 65.3%; Pred. No. 4.3e-46;
Matches 162; Conservative 30; Mismatches 53; Indels 3; Gaps 1;

QY 71 TKLEAPVVVVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSEKIETGGEAITF 130
Db 2 TALTAQVALVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSEKIETGGEAITF 61

QY 131 GGDVSKEADVESMMKAALDKWGTIDVLVNNAGITRDITLLMRKKSQWQDVLDNLTVGVL 190
Db 62 QANVANADEVDQLIKTLDLDFSRIDVLVNNAGITRDITLLMRKKSQWQDVLDNLTVGVL 121

QY 191 CTOAATKVMKRGKIKINIASVVLGTVGVQVQVQVQVQVQVQVQVQV 250
Db 122 CTRVASKLMLKQSGRIINITSVAGWGNFQVQVQVQVQVQVQVQVQV 181

QY 251 NATAPGFIASDMTAELEGELEKILSTIPLGRGQPEVAGLVEFLALNPAASVMTGQVL 310
Db 182 NAVAPGFIATDMTINLNAE---PILQFIPLARYGQPEVAGLVEFLALNPAASVMTGQTF 238

QY 311 TIDGGWVM 318
Db 239 NVDGGWVM 246

RESULT 6
AH2042
3-oxoacyl-[acyl-carrier protein] reductase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2042
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquc
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-251 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAE73593.1; PID:g17130984; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: fabG
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 50.9%; Score 794.5; DB 2; Length 251;
Best Local Similarity 65.0%; Pred. No. 1.1e-45;
Matches 160; Conservative 30; Mismatches 53; Indels 3; Gaps 1;

QY 73 LEAPVVVVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSEKIETGGEAITFGG 132
Db 8 LRQVAVVVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSEKIETGGEAITFGG 67

QY 133 DYSKEADVESMMKAALDKWGTIDVLVNNAGITRDITLLMRKKSQWQDVLDNLTVGVLCT 192
Db 68 DVSQVEQVNDLNGALDKFRDILVNNAGITRDITLLMRKKSQWQDVLDNLTVGVLCT 127

QY 193 QAAATKVMKRGKIKINIASVVLGTVGVQVQVQVQVQVQVQVQVQV 252
Db 128 RAVSKLMLKQSGRIINITSVAGWGNFQVQVQVQVQVQVQVQVQV 187

QY 253 IAPGFIASDMTAELEGELEKILSTIPLGRGQPEVAGLVEFLALNPAASVMTGQVLT 312
Db 188 VAPGFIATDMTINLSE---GILQYIPLARYGQPEVAGLVEFLALNPAASVMTGQVFN 244

QY 313 DGGWVM 318
Db 245 DGGWVM 250

RESULT 7
CB3961
3-oxoacyl-[acyl-carrier protein] reductase fabG [imported] - Bacillus halodurans (stra
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
C;Accession: CB3961
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hi
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans ar
A;Reference number: AB3650; MUID:20512582; PMID:11058132
A;Accession: CB3961
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-246 <STO>
A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAE06210.1; GSPDB:GN
A;Experimental source: strain C-125
C;Genetics:
A;Gene: fabG
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 45.7%; Score 712.5; DB 2; Length 246;

Best Local Similarity 57.7%; Pred. NO. 2.9e-40;
Matches 142; Conservative 41; Mismatches 62; Indels 1; Gaps 1;
QY 73 LEAPVVVTGASRGIGKATATAGKAGCKVLVNYARSSKEAEVSKTEIASGGEAITFGG 132
D 2 LQKTAIVTGAASRGIGRATAMELARHGANGVYVYAGNKEAKVVAEIKELGVEALAIQA 61
QY 133 DVSKEADVESMMKAALDKWGTIDVLVNNAGITRDITLLMRMKKSQWQVIDNLNLTGVFLCT 192
D 62 DVADSESQVAMVKTETIDFGAVIDLVNNAGITRDITLLMRMKKEEDWDVIDNLNLTGVFLCT 121
QY 193 QAATKVMKKGKGIINIASVGLTGNVGOANYSAAGVIGFTKTVAREYASRNINVA 252
D 122 KAVTRPMKQKRGRIINVSVAIGNAGQANYVAKAGVIGLTKLRELANRNITVA 181
QY 253 IAPGFASDMTAEIGEELEKILSTPLGRYQGPVEVAGLVFEFLALNPAASYMTQGVLT 312
D 182 VAPGFETDMTGELPEDVKAQMLGQIPLARLQGPVEVAKVRFLA-SDDASYLTGQTHV 240
QY 313 DGGVMV 318
D 241 NGGMV 246
RESULT 8
A:Accession: A69621
N:Alternate names: 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [validated] - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence revision 05-Dec-1997 #text_change 21-Jul-2000
C:Accession: A69621; PC4176; T46633
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertez
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.F.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, R.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69621
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-246 <KUN>
A:Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13464.1; PID:g2633963
A:Experimental source: strain 168
R:Oguro, A.; Kakeshita, H.; Nakamura, K.; Yamane, K.
Gene 172, 17-24, 1996
A:Title: The effect of Srb, a homologue of the mammalian SRP receptor alpha-subunit, on
A:Reference number: JC4819; MUID:96257247; PMID:8654983
A:Accession: PC4176
A:Molecule type: DNA
A:Residues: 230-246 <OGU>
A:Cross-references: DBJ:D64116; NID:g1389548; PIDN:BAA10974.1; PID:g1237012
R:Cronan, J.E.; Morbidoni, H.R.; de Mendoza, D.
J. Bacteriol. 178, 4794-4800, 1996
A:Title: Bacillus subtilis acyl carrier protein is encoded in a cluster of lipid biosynt
A:Reference number: Z23107; MUID:96326321; PMID:8759840
A:Accession: T46633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22, 'A' 24-246 <CRO>
A:Cross-references: EMBL:U59433; NID:g1502418; PIDN:AAC44307.1; PID:g1502421
A:Experimental source: strain 168
C:Genetics:
A:Gene: fabG; srb

A:Map position: 135-145 degrees
C:Function:
A:Description: EC 1.1.1.100 [validated, MUID:96326321]
A:Pathway: fatty acid biosynthesis
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: fatty acid biosynthesis; NADP; oxidoreductase
F:5-185/Domain: short-chain alcohol dehydrogenase homology <SADH>
F:154/Active site: Tyr #status predicted

Query Match 45.6%; Score 711.5; DB 2; Length 246;
Best Local Similarity 56.9%; Pred. No. 3.4e-40;
Matches 140; Conservative 47; Mismatches 58; Indels 1; Gaps 1;

QY 73 LEAPVVVTGASRGIGKATATAGKAGCKVLVNYARSSKEAEVSKTEIASGGEAITFGG 132
D 2 LNDKTAIVTGAASRGIGRSIALDLAKSGANVYVYAGNEAKANEVVDKSMGRKAIKVA 61
QY 133 DVSKEADVESMMKAALDKWGTIDVLVNNAGITRDITLLMRMKKSQWQVIDNLNLTGVFLCT 192
D 62 DVSNPEDVQNMKIKETLSVFSTIDILVNNAGITRDITLLMRMKKEDEDDVINILNLTGVFLCT 121
QY 193 QAATKVMKKGKGIINIASVGLTGNVGOANYSAAGVIGFTKTVAREYASRNINVA 252
D 122 KAVTRPMKQKRGRIINVSVAIGNAGQANYVAKAGVIGLTKSASAKELASRNITVA 181
QY 253 IAPGFASDMTAEIGEELEKILSTPLGRYQGPVEVAGLVFEFLALNPAASYMTQGVLT 312
D 182 IAPGFISTDMTKLAKDVQDEMLQIPLARFGSPDSVSVVTFIA-SEGARYMTGQTLHI 240
QY 313 DGGVMV 318
D 241 DGGVMV 246

RESULT 9

AG1300
3-ketoacyl-acyl carrier protein reductase homolog fabG [imported] - Listeria monocytog
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AG1300
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloech
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlar
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1300
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99885.1; PID:g16411261; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: fabG
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 44.0%; Score 686.5; DB 2; Length 247;
Best Local Similarity 55.3%; Pred. No. 1.5e-38;
Matches 136; Conservative 42; Mismatches 67; Indels 1; Gaps 1;

QY 73 LEAPVVVTGASRGIGKATATAGKAGCKVLVNYARSSKEAEVSKTEIASGGEAITFGG 132
D 3 LQKVAVVTGSGRGIGRIDAINLAKGANIFFNYNGSPRAAEETAKLVAEHGVEVEMKA 62
QY 133 DVSKEADVESMMKAALDKWGTIDVLVNNAGITRDITLLMRMKKSQWQVIDNLNLTGVFLCT 192
D 63 NVAIEDVDVAFKQAIERFGRVDILVNNAGITRDITLLMRMKKEDEDDVINILNLTGVFLCT 122
QY 193 QAATKVMKKGKGIINIASVGLTGNVGOANYSAAGVIGFTKTVAREYASRNINVA 252
D 123 KAVSRITMKQKRGRIINMASVGLIGNAGQANYVASKAGVIGLTKTTARELAPRGINVA 182

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A;Residues: 1-249 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81497.1; PID:gl5026670; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3574
C;Superfamily: ribitol dehydrogenase, short-chain alcohol dehydrogenase homology

Query Match          42.9%; Score 669.5; DB 2; Length 249;
Best Local Similarity 52.8%; Pred. No. 2.1e-37;
Matches 130; Conservative 50; Mismatches 65; Indels 1; Gaps 1;

QY  73 LEAPVVVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVYSKEIEASGGEAITFGG 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   5 LSGKAVVTGAGRGIGRAITALKLAAGANLVNYSRSEAEQTKLKEIEELGSKAVAVKA 64

QY  133 DYSKEADVESMMKALDKWGIIDVLVNNAGITRDTLLMRMKKSQWQDVIDLNTLGVFLCT 192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   65 DISKYDEAEFTIKKALDEYGTVDLVNNAGITKONLLRMEKEEDFDSVINVLKGAFNCI 124

QY  193 QAATKVMKKRKGKLIINTASVVLGTGNVGQANYSAAGKAGVTFPKTWAREVASNINVNA 252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   125 KITSRVMLKKSGKGLIINSSVGLIGNAGQVNYAAAKAGIIGMTKSKAKEIASRGITVNA 184

QY  253 IAPGFASDMTAEELGEELEKILSTIPLGRYQGPPEVAGLVFEFTALNPAASYMTGQVLT 312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   185 VAPGLIKSDMTDALTDKQRESIAVAVPLNKVGEADVANLVFLA-SDLSSYITGQVINV 243

QY  313 DGGWM 318
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Db   244 DGGWM 249
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RESULT 12
B89896
3-oxoacyl-(acyl-carrier protein) reductase [imported] - *Staphylococcus aureus* (S
C:Species: *Staphylococcus aureus*
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: B89896
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, I.
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu
C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:213111952; PMID:11418146
A:Accession: B89896
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <R>
A;Cross-references: GB:BA000018; PID:g13701031; PIDN:BA842326.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: fabG
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

79	VVTGASRGIGKATALALGKACCKLVNVYASSKEAEVSKEIEASGEATFTFGDVSKEA	138
	8 LVTTGSRGIGRSIALQJAEBSYINVAVYASKEAEAVVEIEKAKGVDSFAIQANADAD	67
	139 DYBSNMKZAALDKWGTIDVLVNNAGITRTDILMRMKKSQOWDVIDNLNTGVFLCTQAAATKV	198
	68 EVKAMIKEVVSQFSGLDVLVNNAGITRDNLNMRMKEQWDDVIDTNLKGVCNCLQKATPQ	127
	139 MMKRRKGGKIINIASVVGLTGNVGQANTSAAKAGVIGFTKTAREYASRNTNVNAIAPGFI	258
	128 MLRQSGAIINLSVVGAVGNPGQANTVATKAGVIGLTKSAARELASRGITVNAVAPGFI	187
	259 ASDMTAEELGELEKKILLSTPLRGYQOPEEVAGLVEFTALNPAASVYMTQGVLLIDGGMV	318
	188 VSDMTDALSDLEKQMLTQPLAFGQDIDIANVAFIA-SDRAKITGTGTHVNGWMY	246

```
RESULT 13
G75333
3-oxoacyl-acyl carrier protein reductase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: G75333
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75333
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-254 <WHI>
A:Cross-references: GB:AE002033; GB:AE000513; NID:g6459726; PIDN:AAF11496.1; PID:g645973
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1943
A:Map position: 1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 41.0%; Score 639.5; DB 2; Length 254;
Best Local Similarity 52.9%; Pred. No. 2.1e-35;
Matches 128; Conservative 43; Mismatches 70; Indels 1; Gaps 1;

QY 75 APVVVVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSKEIEASGGEALTFFGGDV 134
Db 11 ARVALVTGSRGLGRNALRLAQLQPTVAHYHGEBAEQVAADIPRAGGAQVFGADL 70

QY 135 SKRADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDVLDLNLTVFLCTQA 194
Db 71 SQPANAGTLEDVIAALGRDLVLVNNAGITRDLGLAIRMKDEMDVAVLTQLSSAFAACRA 130

QY 195 ATKVMKKKRGKIINIASVVLGTGNVGOANYSAKAGVIGFTKTVAREYASRNINVAIA 254
Db 131 ALKHMKNRSGRIYVNSVVALAGNPGQANYKASGAGLIGLTLALAKYGGRGITVNAIA 190

QY 255 PGFIASDWTAEELGEEKILSTIPLGRYGOPEEVAGLVEFLALNPAASYMTGQVLRTDG 314
Db 191 PGFIESDWTAKLPDXTKKQYQANIPLARFGQPEVALVAFLA-SEGAGVITGQITGVDG 249

QY 315 GM 316
Db 250 GM 251

RESULT 14
F82128
3-oxoacyl- (acyl-carrier-protein) reductase VC2021 [imported] - Vibrio cholerae (strain N
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82128
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: F82128
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <HEI>
A:Cross-references: GB:AB004276; GB:AE003852; NID:g9656555; PIDN:AAF95169.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2021
A:Map position: 1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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```
Query Match 39.8%; Score 621.5; DB 2; Length 248;
Best Local Similarity 51.4%; Pred. No. 3.2e-34;
Matches 127; Conservative 46; Mismatches 67; Indels 7; Gaps 4;

QY 73 LEAPVVVVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSKEIEASG-GEAITFG 131
Db 7 LEGKVALVTGASRGIGKATAEALAEKAKV-IGTATSESGAQAIISDYLGDNGKGMAL--- 62

QY 132 GNVSKRADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDVLDLNLTVFLC 191
Db 63 -NVTNPESIEAVLKAITDFEGGVDILVNNAGITRDLNLRMKKEEWSIDINETNLTISFRL 121

QY 192 TORATKVMKKKRGKIINIASVVLGTGNVGOANYSAKAGVIGFTKTVAREYASRNINVN 251
Db 122 SKAVLDRMMKKRGRIINVSVVGTGNAGQANYAAKAGVIGFTKSMAREVASRGVTVN 181

QY 252 AIAPGFIASDWTAEELGEEKILSTIPLGRYGOPEEVAGLVEFLALNPAASYMTGQVLRT 311
Db 182 TVAPGFIEDWTAKALNDQRTATLAQVPAGRLGDPREIASAVAFLA-SPEAAVITGETLH 240

QY 312 IDGGMVM 318
Db 241 VNGGMVM 247

RESULT 15
F86721
hypothetical protein fabG1 [imported] - Lactococcus lactis subsp. lactis (strain IL14C
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: F86721
R:Belocin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehr
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86721
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <STO>
A:Cross-references: GB:AB005176; PID:g12723693; PIDN:AAK04872.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: fabG1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 39.3%; Score 612.5; DB 2; Length 243;
Best Local Similarity 51.5%; Pred. No. 1.2e-33;
Matches 124; Conservative 44; Mismatches 68; Indels 5; Gaps 2;

QY 78 VVVTGASRGIGKATALALGKAGCKVLVNYARSSKEAEVSKEIEASGGEAITFGDVSK 137
Db 8 VFTVGTGRIGKAIALQFAKAGNLIN--GRSAISEELAEFTAYGVKAVGISGDISKS 65

QY 138 ADVESMMKAALDKWGTIDVLVNNAGITRDTLLMRKKSQWQDVLDLNLTVFLCTQAATK 197
Db 66 EDAAQWVAEAIETLSGVDILVNNAGITRDLGLSLKMEEDPESVLKINLTGAFNMTQAVLK 125

QY 198 VMKKKRGKIINIASVVLGTGNVGOANYSAKAGVIGFTKTVAREYASRNINVAIPGF 257
Db 126 PMTRARSGAIINISVVVLGMENAGQANYAASKAGLIGLTKSIAREVAARNVRVNAVAPGF 185

QY 258 IASDWTAEELGEEKILSTIPLGRYGOPEEVAGLVEFLALNPAASYMTGQVLRTDGMV 317
Db 186 IESDWTAEVLSKVDKADWKAGQIPMKRFGMPPEIATATQFLA---EQEYMTGQVLRTDGMV 242

QY 318 M 318
Db 243 M 243

Search completed: November 7, 2003, 21:04:59
Job time : 27 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 19:34:11 ; Search time 17 Seconds
(without alignments)
879.676 Million cell updates/sec

Title: US-10-024-806-2

Perfect score: 1560

Sequence: 1 MATAAATAAAAVSSPAARG.....NPAASYMTGQVLTIDGMVM 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1130	72.4	320	1	FABG_CUPLA
2	1039.5	66.6	319	1	FABG_AXATH
3	800.5	51.3	247	1	FAGI_SYNY3
4	711.5	45.6	246	1	FABG_BACSU
5	692.5	44.4	201	1	FABG_BRANA
6	621.5	39.8	244	1	FABG_VIBCH
7	592	37.9	246	1	FABG_THEMA
8	584.5	37.5	244	1	FABG_VIBHA
9	576.5	37.0	244	1	FABG_ECOLI
10	575.5	36.9	248	1	FABG_AQUAE
11	574.5	36.8	244	1	FABG_SALTY
12	556	35.6	247	1	FABG_PSEAE
13	545.5	35.0	242	1	FABG_HABIN
14	542.5	34.8	248	1	FABG_CHLMU
15	532.5	34.1	247	1	FABG_CHLTP
16	528	33.8	248	1	FABG_CHLTP
17	508.5	32.6	241	1	FABG_RICPR
18	499.5	32.0	245	1	NODG_RHIS3
19	488.5	31.3	246	1	NODG_AZOBR
20	487.5	31.2	241	1	PHBB_ZOORA
21	473	30.3	261	1	DHG2_BACME
22	471.5	30.2	244	1	FABG_BUCAP
23	468.5	30.0	241	1	PHBB_RHIME
24	464.5	29.8	244	1	FABG_BUCAI
25	464	29.7	246	1	PHBB_CHRVI
26	463	29.7	261	1	DHGA_BACME
27	459.5	29.5	247	1	YD50_MYCTU
28	459	29.4	261	1	DHG3_BACME
29	457	29.3	261	1	DHG4_BACME
30	456.5	29.3	258	1	DHG2_BACSU
31	455.5	29.2	245	1	NODG_RHIME
32	454	29.1	245	1	FABG_BUCBP
33	451	28.9	261	1	DHG_BACSU

34	448.5	28.7	253	1	KDUD_ECOLI
35	447	28.7	248	1	PHAB_ACISP
36	444	28.5	261	1	DHGI_BACME
37	443.5	28.4	255	1	FABG_MYCSM
38	443	28.4	261	1	DHG_BACWE
39	442.5	28.4	240	1	FAG2_SYNY3
40	439.5	28.2	247	1	FABG_MYCTU
41	434.5	27.9	242	1	PHAB_PARDE
42	426.5	27.3	246	1	PHBB_ALCEU
43	425.5	27.3	261	1	ACT3_STRCO
44	423.5	27.1	261	1	DHB8_HUMAN
45	423.5	27.1	262	1	DHGB_BACME

ALIGNMENTS

RESULT 1

ID	FABG_CUPLA	STANDARD;	PRT;	320 AA.
AC	F28643;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	3-oxoacyl-[acyl-carrier protein] reductase, chloroplast precursor			
DE	(EC 1.1.1.100) (3-Ketoacyl-acyl carrier protein reductase).			
GN	CLKR27.			
OS	Cuphea lanceolata.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Myrtales; Lythraceae; Cuphea.			
OX	NCBI_TaxID=3930;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92293104; PubMed=1376402;			
RA	Klein B., Pawlowski K., Hoericke-Grandpierre C., Schell J.,			
RA	Toepfer R.;			
RT	"Isolation and characterization of a cDNA from Cuphea lanceolata			
RT	encoding a beta-ketoacyl-ACP reductase.";			
RL	Mol. Gen. Genet. 233:123-128(1992).			
CC	-!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +			
CC	NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH			
CC	-!- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.			
CC	-!- SUBUNIT: Homotetramer (Probable).			
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC			
CC	PLASTIDS.			
CC	-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases			
CC	(SDR) family.			

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EMBL; X64566; CAA45866.1; -	
PIR; S22450; S22450.	
HSSP; P50162; 1A81.	
InterPro; IPR002198; ADH_short.	
Pfam; PF00106; adh_short; 1.	
PRINTS; PRO0080; SDRFAMILY.	
PROSITE; PS00061; ADH_SHORT; 1.	
Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;	
Transit peptide.	
TRANSIT	1 61
CHAIN	62 320
NP_BIND	82 106
ACT_SITE	227 227
SEQUENCE	320 AA; 33103 MW; 06BAF0522B2B8C87 CRC64;

RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Togmon A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Wiari A., Wambutt R., Wedler E., Wedler H., Weitzneger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*.";
 RL Nature 390:249-256 (1997).
 RN [3]
 RP SEQUENCE OF 1-172 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98195738; PubMed=9534248;
 RA Poulger D., Errington J.;
 RT "A 28 kbp segment from the *spovm* region of the *Bacillus subtilis* 168
 RL genome.";
 RN Microbiology 144:801-805 (1998).
 RP [4]
 RP SEQUENCE OF 230-246 FROM N.A.
 RC STRAIN=168;
 RA Oguro A., Kakeshita H., Takamatsu H., Nakamura K., Yamane K.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
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 CC -----
 DR EMBL; U59433; AAC4307.1; -;
 DR EMBL; Z99112; CAB13464.1; -;
 DR EMBL; Y13937; CAA74250.1; -;
 DR EMBL; D64116; BAA10974.1; -;
 DR PIR; A69621; A69621.
 DR HSP; Q12634; 1YBV.
 DR Subtilist; BG11535; fabg.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; FALSE NEG.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 9 33
 FT ACT_SITE 154 154
 FT CONFLICT 23 23
 FT D -> A. (IN REF. 1).
 FT SEQUENCE 246 AA; 26282 MW; 26282 MW; C6A391167D3237DC CRC64;
 Query Match 45.6%; Score 711.5; DB 1; Length 246;
 Best Local Similarity 56.9%; Pred. No. 2e-38;
 Matches 140; Conservative 47; Mismatches 58; Indels 1; Gaps 1;
 QY 73 LEAPVVVVTGASRGIGKATLALGKAGCKVLVNYARSKAEVSKSEIRASGGEAITFGG 132
 DB 2 LNDKTAIVTGSAGRIGRSIALDLAKSGANVYVSGNEAKANEVVDSEIKSGRAIAVKA 61
 QY 133 DVSKAEAVESNMKALDKNGTIDVYVNNAGITRTILMRKKSQWQVIDNLNLTGVFLCT 192
 DB 62 DVSNFEDVQNMKEKTLVSFSTIDILVNNAGITRNLNMRKEDWDVVDVNLKGVFNCT 121
 QY 193 QATKVMKMKRKGKIIINIASVVGTVGNVGOANYSAAGVIGTKTVAREYASRNINVA 252
 DB 122 KAVTRQMKQKQSGRIINVSIVGVSGNPGQANYVAAGVIGLTKSSAKELASRNITVA 181
 QY 253 IAPGFASMTAEAGEELEKKILSTIFLGRYGQPEEVAGLVFLALNPAASVMTQVLTI 312
 DB 182 IAPGFISTDNTDKLADVQDEMLKQIPLARFGEPSDVSVVTFLA-SEGARYMTGQTLHI 240
 QY 313 DGGNVM 318

DB 241 DGGNVM 246
 RESULT 5
 FABG_BRANA
 ID FABG_BRANA STANDARD; PRT; 201 AA.
 AC P27582;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase [EC 1.1.1.100] (3-ketoacyl-
 DE acyl carrier protein reductase) (Fragments).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE OF 35-62 AND 81-84.
 RC TISSUE=Seed;
 RX MEDLINE=92223071; PubMed=1562581;
 RA Sheldon P.S., Kekwick R.G.O., Smith C.G., Sidebottom C.M.,
 RA Slabas A.R.;
 RT "Molecular cloning of higher-plant 3-oxoacyl-[acyl carrier protein]
 RT reductase. Sequence identities with the nodG-gene product of the
 RT nitrogen-fixing soil bacterium *Rhizobium meliloti*.";
 RL Biochem. Biophys. Acta 1120:151-159 (1992).
 RN [2]
 RP SEQUENCE OF 63-201 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=92246853; PubMed=1575676;
 RA Slabas A.R., Chase D., Nishida I., Murata N., Sidebottom C.,
 RA Safford R., Kekwick R.G., Sheldon P.S., Hardie D.G., Mackintosh R.W.;
 RT "Molecular cloning of higher-plant 3-oxoacyl-[acyl carrier protein]
 RT reductase. Sequence identities with the nodG-gene product of the
 RT nitrogen-fixing soil bacterium *Rhizobium meliloti*.";
 RL Biochem. J. 283:321-326 (1992).
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC -1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
 CC -1- SUBUNIT: Homotetramer (Probable).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
 CC PLASTIDS.
 CC -1- TISSUE SPECIFICITY: EMBRYO AND LEAF TISSUES.
 CC -1- MISCELLANEOUS: EXHIBITS A MARKED PREFERENCE FOR ACYL-CARRIER
 CC PROTEIN DERIVATIVES OVER COA DERIVATIVES AS SUBSTRATES.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X64463; CAA45793.1; -;
 DR PIR; S22417; S22417.
 DR HSP; P50162; 1AE1.
 DR InterPro; IPR002198; ADH_short.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast.
 FT NON_CONS 27 28
 FT NON_CONS 34 35
 FT NON_CONS 62 63
 FT ACT_SITE 108 108
 FT BY SIMILARITY.
 FT SEQUENCE 201 AA; 21042 MW; FD51B2E369D2D967 CRC64;
 Query Match 44.4%; Score 692.5; DB 1; Length 201;
 Best Local Similarity 57.8%; Pred. No. 2.5e-37;
 Matches 149; Conservative 23; Mismatches 27; Indels 59; Gaps 3;

Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the *Escherichia coli* K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
[4]
SEQUENCE FROM N.A.
SPECIES=flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
Yu J.;
"Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
through comparison with genomes of *Escherichia coli* K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.

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EMBL; M84991; AAA23739.1; -
EMBL; AE000210; AAC74177.1; -
EMBL; D90745; BAA35901.1; -
EMBL; AE015136; AAN42716.1; -
PIR; B64853; B42147.
PDB; 1I01; 2I-DEC-01.
Ecogen; EG11318; fabG.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome;
KW 3D-structure.
FT NP_BIND 10 34 NADP (BY SIMILARITY).
FT ACT_SITE 151 151 BY SIMILARITY.
FT CONFLICT 30 30 A -> G (IN REF. 1).
FT SEQUENCE 244 AA; 25560 MW; 48EC1F2A77EEFD9 CRC64;

Query Match 37.0%; Score 576.5; DB 1; Length 244;
Best Local Similarity 49.4%; Pred. No. 6.7e-30;
Matches 121; Conservative 45; Mismatches 74; Indels 5; Gaps 3;
QY 74 EAPVVVVTGASRGIGKATALGKAGKVLVNYARSSKEAEVSKVE--IEASGGE 133
DB 4 EGKIALVVTGASRGIGKATALGKAGKVLVNYARSSKEAEVSKVE--IEASGGE 59
QY 134 VSKEADVESMKAAALDKWGTIDVLVNNAGITDRLMLMKKSQMDVLDNLGTGVLCTQ 193
DB 60 VTPDASIESVLEKIRAEFEVDILVNNAGITDRLMLMKKSQMDVLDNLGTGVLCTQ 119
QY 194 AATKVMKKRKGKINIASVGLTGNVGOANYSAAGVIGFTKTVAREYASRNINVAI 253
DB 120 AVNRAMKKRRHRIITIGSWGTMGNGGQANYAAKAGLIGFSKSLAREVASRGITNVV 179
QY 254 ACGFIASDWTAELEGELEKILSTPLGRYGOPEVAGLVEFLALNPAASITMTQVLTID 313
DB 180 APGFIEDTRALSDQDAGILAQVPAAGLGAQBIANAVAFASDEAA-YITGETLHVN 238
QY 314 GGMVM 318
DB 239 GGMVM 243

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RESULT 11
FABG_SALTY STANDARD; PRT; 244 AA.
ID O85141;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR STM1195 OR STY1234 OR T1725.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2;
RX MEDLINE=98317265; PubMed=9642179;
RA Zhang Y., Cronan J.E. Jr.;
RT "Transcriptional analysis of essential genes of the Escherichia coli
RT fatty acid biosynthesis gene cluster by functional replacement with
RT the analogous Salmonella typhimurium gene cluster.";
RL J. Bacteriol. 180:3295-3303(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kocoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC
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CC CC
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CC DR EMBL; AF044668; AAC38650.1; -
CC DR EMBL; AB008752; AAL20124.1; -
CC DR EMBL; AL627269; CAD08319.1; -
CC DR EMBL; AS016839; AAC069349.1; -
CC DR HSSP; P19992; IHDC.
CC DR StyGene; SGI0638; fabG.
CC DR InterPro; IPR002198; ADH short.
CC DR Pfam; PF0106; adh short; 1.
CC DR PRINTS; PR00080; SDRFAMILY.
CC DR PROSITE; PS00061; ADH_SHORT; 1.
CC KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
CC FT NP_BIND 10 34 NADP (BY SIMILARITY).
CC FT ACT_SITE 151 151 BY SIMILARITY.
CC SQ SEQUENCE 244 AA; 25545 MW; 86D71DA3E9AF0363 CRC64;

Query Match 36.8%; Score 574.5; DB 1; Length 244;
Best Local Similarity 49.4%; Pred. No. 8.9e-30;
Matches 121; Conservative 45; Mismatches 74; Indels 5; Gaps 3;

QY 74 EAPVVVVTGASRGIGKATALGKAGCKVLNVVARSKEAEVSKIEASGGEAIFGCD 133
Db 4 EKKIALVTGASRGIGKATALGKAGCKVLNVVARSKEAEVSKIEASGGEAIFGCD 133
QY 134 VSKEADVESMKAALDKWTIDVLVNNAGITRTDILMRMKSQWQVDILNLTGVFLCTQ 193
Db 60 VTDPASIESVLEIRAEFGVDILVNNAGITRTDILMRMKQDDEWNDIETNLSVFLSK 119
QY 194 AATKVMKKKIKINIASVGLTGNVGOANYSAKAGVIGTKTVARYAGRNINVAI 253
Db 120 AVNRAMKKKCRITITIGSWGTMGNAGQAAKAGLIGFSKSLAREVASRGITVVV 179
QY 254 AFGFTASDMTAEILGEEKILSTIPLGRYGOPEEVAGVVEFLANPARSVMTGQVLTID 313
Db 180 AFGFTETDTRALSDDQRAIGLAQVPAKLGAGQETASAVFLA-SDEASYITGETLHVN 238
QY 314 GGVNM 318
Db 239 GGVNM 243

RESULT 12
FABG_PSEAE STANDARD; PRT; 247 AA.
ID FABG_PSEAE
AC O54438;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR PA2967.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=99395062; PubMed=10464226;
RA Kutchna A.J., Hoang T.T., Schweizer H.P.;
RT "Characterization of a Pseudomonas aeruginosa fatty acid biosynthetic
RT gene cluster: purification of acyl carrier protein (ACP) and malonyl-
RT coenzyme A:ACP transacylase (fabD).";
RL J. Bacteriol. 181:5498-5504(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,

```



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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR TC0508.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Ni99;
RX MEDLINE=20150255; PubMed=10694935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heideberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Barry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT 'Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.';
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -|- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -|- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -|- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
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CC -----
CC EMBL: AF002319; AAF39350.1; -.
CC PIR: E81695; E81695.
CC HSSP: P50163; 2AE1.
CC TIGR: TC0508; -.
CC InterPro: IPR002198; ADH_SHORT; 1.
CC Pfam: PF00106; adh_short; 1.
CC PRINTS: PR00080; SDRFAMILY.
CC PROSITE: PS00061; ADH_SHORT; 1.
CC Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
CC FT NP BIND 12 36 NADP (BY SIMILARITY).
CC ACT_SITE 157 157 BY SIMILARITY.
CC SEQUENCE 248 AA; 25977 MW; 1F5C8968CB05FF58 CRC64;
CC -----
Query Match 34.8%; Score 542.5; DB 1; Length 248;
Best Local Similarity 46.9%; Pred. No. 9.6e-28;
Matches 112; Conservative 47; Mismatches 77; Indels 3; Gaps 3;
QY 79 VVTGASRGIGKATALGKAGCKVLVNYARSSKEAEVSKTEASGGEATFG-GDVSKE 137
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
11 IVTGGSGIGFGIAKLFAEAGANVQI-WGINEAGKSAADLSKDTGSKVSPALVDVSKN 69
QY 138 ADVESMMKALDKWTIDVLVNNAGITRDTLLMRKKSQWQVDIDNLTVGFLCTQAAATK 197
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70 DMVSAQVQKFLARYGIDVNVNAGITRDSLLMRMSEEESSVIDNLGSIYNVCSAVIR 129
QY 198 VMKKRKGKIIINIASVGLTGNVQANYSAAGKGVGFTKTVAREVASNNINVAIPGF 257
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
130 PMTKARSGAINISSIVGLRSGPGQNTYAAAGAGIIGFSKALSKVSGKNIRVNCIAPGF 189
QY 258 IASDMTAEELGEEKILSTIPLGRYGOPEEVLGVEFLALNPAASVMTGVLTIIDGGM 316
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
190 IDTDMTKGLSDNLKNEWLKGVPLGRVTPTEPIIAAALFLASN-QSSYITGQVLSVDGGM 247
RESULT 15
FABG CHLTR
ID_FABG CHLTR STANDARD; PRT; 247 AA.
AC P38004; O84240;
DT 01-OCT-1994 (Rel. 30, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
DE acyl carrier protein reductase).
GN FABG OR CT237.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/CX;
RX MEDLINE=99000809; PubMed=97841136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT 'Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.';
RL Science 282:754-759(1998).
RN [2]
RP SEQUENCE OF 1-10 FROM N.A.
RC STRAIN=L2/434/Bu;
RA Binl L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -|- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -|- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
CC -|- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE001297; AAC67830.1; -.
CC PIR: F71538; F71538.
CC HSSP: P47227; 1BDB.
CC Siema-2DPAGE; P38004; -.
CC InterPro: IPR002198; ADH_SHORT.
CC Pfam: PF00106; adh_short; 1.
CC PRINTS: PR00080; SDRFAMILY.
CC PROSITE: PS00061; ADH_SHORT; 1.
CC Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
CC FT INIT MET 0 0
CC NP_BIND 11 35 NADP (BY SIMILARITY).
CC ACT_SITE 156 156 BY SIMILARITY.
CC CONFLICT 2 2 G -> T (IN REF. 2).
CC SEQUENCE 247 AA; 25888 MW; F98A1F17264F4EC1 CRC64;
CC -----
Query Match 34.1%; Score 532.5; DB 1; Length 247;
Best Local Similarity 46.0%; Pred. No. 4.1e-27;
Matches 110; Conservative 47; Mismatches 79; Indels 3; Gaps 3;
QY 79 VVTGASRGIGKATALGKAGCKVLVNYARSSKEAEVSKTEASGGEATFG-GDVSKE 137
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
10 IVTGGSGIGFGIAKLFAEAGANVQI-WGINEAGKSAADLSKDTGSKVSPALVDVSKN 68
QY 138 ADVESMMKALDKWTIDVLVNNAGITRDTLLMRKKSQWQVDIDNLTVGFLCTQAAATK 197
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
69 DMVSAQVQKFLARYGIDVNVNAGITRDSLLMRMSEEESSVIDNLGSIYNVCSAVIR 128
QY 198 VMKKRKGKIIINIASVGLTGNVQANYSAAGKGVGFTKTVAREVASNNINVAIPGF 257
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
129 PMTKARSGAINISSIVGLRSGPGQNTYAAAGAGIIGFSKALSKVSGKNIRVNCIAPGF 188
QY 258 IASDMTAEELGEEKILSTIPLGRYGOPEEVLGVEFLALNPAASVMTGVLTIIDGGM 316
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
189 IDTDMTKGLSDNLKNEWLKGVPLGRVTPTEPIIAAALFLA-SDGSSYITGQVLSVDGGM 246
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Search completed: November 7, 2003, 21:03:19
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: November 7, 2003, 20:49:21 ; Search time 60 Seconds

(without alignments)
1367.679 Million cell updates/sec

Title: US-10-024-806-2

Perfect score: 1560

Sequence: 1 MATAAATAAAAVSSPAARG.....NPASVMTGQVLTIDGGVMV 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL 23:**

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1093	70.1	315	10	Q949M3
2	1093	70.1	320	10	Q93X62
3	1078.5	69.1	328	10	Q93X67
4	1068	68.5	317	10	Q93X68
5	1040.5	66.7	254	10	Q949M2
6	794.5	50.9	251	16	Q8VY70
7	777.5	49.8	245	16	Q8DLS9
8	712.5	45.7	246	16	Q9KA03
9	701.5	45.0	246	16	Q8ER07
10	700.5	44.9	257	2	Q8GE35
11	686.5	44.0	247	16	Q8V690
12	681.5	43.7	247	16	Q92AK1
13	674.5	43.2	247	16	Q8R9W0
14	669.5	42.9	249	16	Q97DA6
15	659.5	42.3	246	16	Q8X1H1
16	658.5	42.2	246	16	Q99QK7

17	647.5	41.5	244	16	Q8CPI3
18	639.5	41.0	254	16	Q9RT26
19	626	40.1	254	16	Q8EXX5
20	619	39.7	301	5	Q8I2S7
21	614	39.4	301	5	Q965D6
22	612.5	39.3	243	16	Q9CHP7
23	611.5	39.2	248	16	Q8D8G8
24	597.5	38.3	243	16	Q8DRI5
25	596.5	38.2	243	16	Q9FBC3
26	595.5	38.2	244	16	Q8NZN2
27	595.5	38.2	244	16	Q8K628
28	591	37.9	245	16	Q8KAP0
29	590.5	37.9	248	16	Q8EDH3
30	587.5	37.7	244	16	Q99YD6
31	580.5	37.2	244	16	Q8E723
32	580.5	37.2	244	16	Q8E1K6
33	576	36.9	247	16	Q8PB09
34	573.5	36.8	244	16	Q8X3I5
35	571	36.6	247	16	Q9PFI6
36	567	36.3	247	16	Q8PNE4
37	559	35.8	248	16	Q9JXR1
38	559	35.8	248	16	Q9JW61
39	558.5	35.8	244	16	Q8ZFT5
40	558.5	35.8	244	16	Q8DSN5
41	554	35.5	247	2	Q8GI82
42	549	35.2	249	16	Q8Y0J2
43	545.5	35.0	247	16	Q9PI70
44	544.5	34.9	242	16	Q9CJS6
45	537.5	34.5	244	2	Q9RA33

ALIGNMENTS

RESULT 1

Q949M3 PRELIMINARY; PRT; 315 AA.
AC Q949M3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 3-oxacyl-[acyl carrier protein] reductase (EC 1.1.1.100).
GN BKE3
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
CX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RA McDonald F.S., White A.J., Elborough K.M., Slabas A.R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL: AJ243085; CAC41364.1; -;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 315 AA; 33140 MW; 3B0B36C94A4FB313 CRC64;

Query Match 70.1%; Score 1093; DB 10; Length 315;
Best Local Similarity 80.7%; Pred. No. 2.3e-56;
Matches 213; Conservative 28; Mismatches 23; Indels 0; Gaps 0;
QY 55 VQTHAAVQAVVVDATKLEAPVVVTGASRGIGKATALGAGCKLVNYSARSKAE 114
Db 52 VKQAATAVEAGTGEAPVKVESPVVVVTGASRGIGKATALGAGCKLVNYSARSKAE 111
QY 115 EVSKTEASGGEAITGGVSKAEADYVESNMKALDKWIDVLVNNAGITRDTLLRMKK 174
Db 112 EVSKQIEAGGQAITGGVSKAEADYVESNMKALDKWIDVLVNNAGITRDTLLRMKK 171

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QY 175 SQWQVVIDNLNLTGVFLCTQATKMMKKRGKIIINIASVVLGNTGNVGOANYSAKAGVIG 234
DB 172 SQWDEVIDNLNLTGVFLCTQATKMMKKRGKIIINIASVVLGNTGNVGOANYSAKAGVIG 231
QY 235 PFTKTVAREASRNINNVNAPGFIASDMTAELEKILSTIPLGRYQGPVEVAGLVE 294
DB 232 PSKTAAREGASRNINNVNVCPIASDMTAKIGEDMEKKILSTIPLGRYQGPVEDVAGLVE 291
QY 295 FLALNPAASVMTQVLTIDGGMW 318
DB 292 FLALSPAASVMTQVLTIDGGMW 315

RESULT 2
Q93X62 PRELIMINARY; PRT; 320 AA.
AC Q93X62;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Beta-oxacyl-[acyl-carrier protein] reductase (EC 1.1.1.100).
GN GBKRI.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP TISSUE=Leaf;
RC McDonald F.S., White A.J., Elborough K.M., Slabas A.R.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AJ243091; CAC41370.1; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 320 AA; 33671 MW; 3D79CEA41AFFBC49 CRC64;

Query Match 70.18; Score 1093; DB 10; Length 320;
Best Local Similarity 80.78; Pred. No. 2.3e-56;
Matches 213; Conservative 28; Mismatches 23; Indels 0; Gaps 0;

QY 55 VQTHVAAREQAVVVDATKLEAPVTVGASRGIGKATALGKAGCKVLNVARSKEAE 114
DB 57 VKAQATAVEQSTGEAVKVPVSPVTVGASRGIGKATALGKAGCKVLNVARSKEAE 116
QY 115 EVSKEIASGGEALTFGDVSKEADVESMMKALDKWGTIDVLVNNAGITRDTLLMRKK 174
DB 117 EVSKEIASGGEALTFGDVSKEADVESMMKALDKWGTIDVLVNNAGITRDTLLMRKK 176
QY 175 SQWQVVIDNLNLTGVFLCTQATKMMKKRGKIIINIASVVLGNTGNVGOANYSAKAGVIG 234
DB 177 SQWDEVIDNLNLTGVFLCTQATKMMKKRGKIIINIASVVLGNTGNVGOANYSAKAGVIG 236
QY 235 PFTKTVAREASRNINNVNAPGFIASDMTAELEKILSTIPLGRYQGPVEVAGLVE 294
DB 237 PSKTAAREGASRNINNVNVCPIASDMTAKIGEDMEKKILSTIPLGRYQGPVEDVAGLVE 296
QY 295 FLALNPAASVMTQVLTIDGGMW 318
DB 297 FLALSPAASVMTQVLTIDGGMW 315

RESULT 3
Q93X67 PRELIMINARY; PRT; 328 AA.
AC Q93X67;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)

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DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE 3-oxacyl-[acyl carrier protein] reductase (EC 1.1.1.100).
GN BKR2.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA McDonald F.S., White A.J., Elborough K.M., Slabas A.R.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AJ243084; CAC41363.1; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase.
SQ SEQUENCE 328 AA; 34373 MW; AFB61AF1C665545F CRC64;

Query Match 69.18; Score 1078.5; DB 10; Length 328;
Best Local Similarity 73.48; Pred. No. 1.7e-55;
Matches 215; Conservative 31; Mismatches 32; Indels 15; Gaps 2;

QY 28 SRRGFVTFGGGAARFSEFLRSRGFGVQTHVAAREQAVVVDK--ATKLEAPVTVVVGASR 85
DB 49 SRRPFATSSSTVVQ-----AQQAATAEQSTGEAEVAPKVPVTVVVGASR 95
QY 86 GIGKATALGKAGCKVLNVARSKEAEVSKIEIASGGEALTFGDVSKEADVESMMK 145
DB 96 GIGKATALGKAGCKVLNVARSKEAEVSKIEIASGGEALTFGDVSKEADVESMMK 155
QY 146 AALDKWGTIDVLVNNAGITRDTLLMRKKSQWQVVIDNLNLTGVFLCTQATKMMKKRG 205
DB 156 TVDANGTIDVLVNNAGITRDTLLMRKKSQWQVVIDNLNLTGVFLCTQATKMMKKRG 215
QY 206 KIINIASVVLGNTGNVGOANYSAKAGVIGFTKTVAREASRNINNVNAPGFIASDMTAE 265
DB 216 KIINIASVVLGNTGNVGOANYSAKAGVIGFTKTVAREASRNINNVNVCPIASDMTAK 275
QY 266 LGELEKILSTIPLGRYQGPVEVAGLVEFLALNPAASVMTQVLTIDGGMW 318
DB 276 LGEDMEKKILSTIPLGRYQGPVEDVAGLVEFLALSPAASVMTQVLTIDGGMW 328

RESULT 4
Q93X68 PRELIMINARY; PRT; 317 AA.
AC Q93X68;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE 3-oxacyl-[acyl-carrier protein] reductase (EC 1.1.1.100).
DE (Fragment).
GN BKR1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA McDonald F.S., White A.J., Elborough K.M., Slabas A.R.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL; AJ243083; CAC41362.1; -.
DR InterPro; IPR002198; ADH_short.

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RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain FCC 7120." ;
RL DNA Res. 8:203-213 (2001).
RL EMBL; AP003587; BAB73593.1; -.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF001106; adh_short_1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR Complete proteome.
KW KW
SQ SEQUENCE 251 AA; 26218 MW; 57D0712F8EA6B698 CRC64;

      Query Match          50.9%; Score 794.5; DB 16; Length 251;
      Best Local Similarity 65.0%; Pred No. 4.5e-39;
      Matches 160; Conservative 30; Mismatches 53; Indels 3; Gaps 1

QY 73 LEAPVVVTGASRGIGKATALAGKAGCKVLVNYARSKEAEVRSKEIEASGGEATFGG 132
Db 8 LRQGVAVVTGASRGIGRAIALELANYGATVVVNYASSSTADEVVAEITGAGGEAVLKA 67

QY 133 DVSKEADVESNMKKAALDKWGTIDVLVNNAGITDITLLMNMKKSQWODVIDLMLTGVF 192
Db 68 DVSQVEQVDNLIINGAIDKFRIIDILVNNAGITDITLLRMKPDWQAOVIDLMLTGVF 127

QY 193 QAAQVNMVKKRKGKIIINIASVGLTGNVGQANYSAAKAGVIGTKTVAREYASRNINVA 252
Db 128 RAVSKMLMKQBSGRINIITVAGQMGNPGQANYSAAKAGVIGTKTVAKELASRGITVNA 187

QY 253 IAPGFASDMTAEIGEELEKKILSTIPLRGYGOPEEVAGIVLEFLALNPAASYMTGVLTI 312
Db 188 VAPGFATDMTSLNKSE---GILQYIPLRGYGOPEEIVAGVWVFLAADPAAAVITGQVFN 244

QY 313 DGGVMV 318
Db 245 DGGVMV 250

RESULT 7

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QY	193	QAATKVMKKRKGKIINIASVGLTGNVGQANYSAAGAVIGFTKTVAEAYASRNINVNA	255
Dd	122	KAVTRGMQKGRRIINVASIVGSGNPGQANVAAKAGVIGLTKTSAKELASRNILVNA	181
QY	253	IAPGFIASDMTAELGELEBKILSTIPLRGYQPPEVAGLVREFLAINPAASYMTGOVLTI	312
Dd	182	VAPGFISTDMDTLQSKSQDLSLLSVLFERFGKPEDVARVRVRFATED-ANYITGTTHI	240
QY	313	DGGWMV 318	
Dd	241	DGGWMV 246	
 RESULT 10 Q8GE35 PRELIMINARY; PRT; 257 AA.			
ID	Q8GE35;		
AC	O8GE35;		
DT	01-MAR-'2003 (TREMBLrel. 23, Created)		
DT	01-MAR-'2003 (TREMBLrel. 23, Last sequence update)		
DT	01-MAR-'2003 (TREMBLrel. 23, Last annotation update)		
DE	3-oxoacyl-[acyl-carrier protein] reductase [EC 1.1.1.100]		
DE	(Fragment).		
OS	Heliobacillus mobilis.		
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae;		
OC	Heliobacillus.		
CX	NCBI_TaxID=28064;		
RX	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22337798; PubMed=12446909;		
RA	Raymond J.; Zhaxybayeva O., Gogarten J.P., Gerdes S.Y.,		
RA	Blankenship R.E.;		
RT	"Whole-genome analysis of photosynthetic prokaryotes.";		
RL	Science 238:1616-1620(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Liolios K.G., Chu L., Ostrovskaya O., Mendybaeva N., Koukharenko V.,		
RA	Gerdos S., Kyripides N., Overbeek R.;		
RL	Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AY142784; AAN87388.1; -		
KW	Oxidoreductase.		
FT	NON TER 257		
SQ	SEQUENCE 257 AA; 27163 MW; C68CFSC5AE77C2F7 CRC64;		
 Query Match 44.9%; Score 700.5; DB 2; Length 257; Best Local Similarity 56.0%; Pred. No. 1.4e-33; Matches 140; Conservative 43; Mismatches 66; Indels 1; Gaps 17			
QY	69	DATKLEAPVVVTGASRGIGKATALAGKGVUNVYARSKEAEVSKIEASGGBAI	128
Dd	8	DKMGVDLTALVTGASRGIGKAIALQLAADGFAVANVYAGSEAKANEVVEBIIISAGGKAF	67
QY	129	TFGDVSKAEADVESNMKAALDKWTGDIVLVNNAGTTTRDTLARMKKCSOWQDVIDNLTCV	188
Dd	68	AIQGDVSRSDDQVENWQKVLAEPGRIDIVLVNNAGITRDNLMLRKLBEDWDVLDPTNLKGL	127
QY	189	FLCTQAATKVMKKRKGKIINIASVGLTGNVGQANYSAAGAVIGFTKTVAEAYASRN I	248
Dd	128	FLCSAIKPWKQRSGRINIITSVWGMMGAGQNYAAAAGVIGLTKYLAKELGSNI	187
QY	249	NVNAIARGFTASDMTAELGELEBKILSTIPLRGYQPPEVAGLVREFLAINPAASYMTGO	308
Dd	188	TVNAAVAFGYIOTDMDTKLSDVRESLAKITIPLRGLOPQEDVAKVVAFLA-SESAKITQG	246
QY	309	VLTIIDGGWMV 318	
Dd	247	TINVDGGWMV 256	
 RESULT 11 Q8Y690 PRELIMINARY; PRT; 247 AA.			
ID	Q8Y690		
AC	Q8Y690;		
DT	01-MAR-'2002 (TREMBLrel. 20, Created)		

[illegible]

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RESULT 13
Q8R9W0
ID Q8R9W0 PRELIMINARY; PRT; 247 AA.
AC Q8R9W0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Dehydrogenases with different specificities (Related to short-chain
DE alcohol dehydrogenases).
DE FABG3 OR TTE1472
GN FABG3
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11937336;
RA Bao Q., Tian Y., Li W., Xu Z., Huang L., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AB013105; AAM24694.1; -.
DR InterPro; IPR002198; ADH short.

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[illegible]

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RESULT 14
Q97DA6
ID ID Q97DA6 PRELIMINARY; PERT; 249 AA.
DC Q97DA6;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 3-ketoacyl-acyl carrier protein reductase.
GN GAC3574.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838 (2001).
DR EMBL; AB007854; AAK81497.1; -.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Complete proteome.
SQ SEQUENCE 249 AA. 26247 MW. B13D7EDAC21A626A CRC64:

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Query Match      42.9%; Score 669.5; DB 16; Length 249;
Best Local Similarity 52.8%; Pred.No.8.9e-32;
Matches 130; Conservative 50; Mismatches 65; Indels 1; Gaps 1;

QY 73 LEAPVVVTGASRGIGKATALGAGCKVLVNYARSRSKEAEVSEKIEIASGCEATTFGG 132
DB 5 LSGKVAVVTGAGRLGTAIALKLAEGANLVVNYRSSSAETOKLKEIEELGSKAVAVKA 64

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QY	133	DVSKEADVESMKAALDKWGTIDVLVNNAGITRDTILMRMKKSQWQDVIDLALTGVLCT	192
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	65	DISKYDEAETIIKKALDSYGIVDILVNNAGITKDNILLRMKEDFDSVINVLKGAFNCI	124
		: : : : : : : : : : : : : : : : : : : : : : : : :	
QY	193	QAATKVMKKRGKGIINTASVVLGTGNVGQANYSAKAGVIGTKTVAREYASRNINVA	252
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	125	KHTRVWLKCKSGKGIINSSVIGLIGNAGQVNYAAAKAGIIGMTKSVAKELASRGITVNA	184
		: : : : : : : : : : : : : : : : : : : : : : : : :	
QY	253	IAPGTASDMTAELEKXILSTIPIGRYGPQPEEVAGLVFELALNPAASVYNTGVLT	312
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	185	VAPGIKSDMTDALTDKQRESIVAAVPLNKVGEAEDVANLVFLA-SDLSSVYITGVQVNV	243
		: : : : : : : : : : : : : : : : : : : : : : : : :	
QY	313	DGMVM 318	
Db	244	DGMVM 249	

RESULT	ID	PRELIMINARY;	PRT;	246 AA.
08XLIH1	08XLIH1			
AC	01-WAR-2002 (TREMELrel. 20, Created)			
DT	01-WAR-2002 (TREMELrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMELrel. 21, Last annotation update)			
DE	3-oxoacyl-l-acyl-carrier-protein[reductase.			
DE	FABG OR CPB1070.			
OS	Clostridium perfringens.			
OS	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			
OC	Clostridium			
OC	Clostridium			
OX	NCBI_TaxID=1502;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=13 / Type A;			
RC	PubMed=11792842;			
RX	Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,			
RA	Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;			
RA	"Complete genome sequence of Clostridium perfringens, an anaerobic			
RT	flesh-eater.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).			
RL	EMBL; AF003189; BAB80776.1; "-			
DR	InterPro; IPR002198; ADH short.			
DR	Pfam; PF00106; adh short; 1.			
DR	PRINTS; PR00080; SDRFAMILY.			
DR	PROSITE; PS00061; ADH_SHORT; 1.			
DR	Complete proteome.			
XM	SEQUENCE 246 AA. 26267 MW; CD90B8C650ECC817 CRC64;			
SQ				

Query Match	42.3%;	Score	659.5;	DB	16;	Length	246;		
Best local Similarity	52.8;	Pred. No.	3.4e-31;						
Matches	130;	Conservative	48;	Mismatches	67;	Indels	1;	Gaps	1;
Qy	73	LEAPVVVVVTGASRGIGKATALGKAGCKVLVINYARSSKEAEVSKETIASGGEAIFGG	132						
Db	2	LKDQVAIVTGGTRGIGRAIALKLADQGANIVYRNRSQKEAEULKEEGVKVLTKVC	61						
Qy	133	DVSKAEADVESNMKAALDKWGTIDVLVNNAGTTRDTLLMRMKKSQWQDVIDLNTGVPLCT	192						
Db	62	DISNFEDSKMLMDKCEKVFQKIDILVNNAGTIDKDTLLMRMKEDFDNDVIDVNLKGFNCA	121						
Qy	193	QAATKVMKRRKGKIIINIASVVGTLTNGVQANYSAAGAGVIGFTKTIVAREVASRNINVA	252						
Db	122	KHSAIAMLKQRFQKIIINNTSVVGIAGNAGQVNYSAKAGVIGLTKSLAKELGSRGITVNA	181						
Qy	253	IAPGFASIDMTAEELGEELEKILSTIPLGRVQGPREEVAGLVEFLALNPAAASYMVGVLTI	312						
Db	182	VAPGFIINDMTASUSEKVEASXNPIPKRLGDEPDVANLVGFUA-SDAAIYITGQVINV	240						
Qy	313	DGGMYM	318						
Db	241	DGGMYM	246						

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 13:14:24 ; Search time 5004 Seconds
(without alignments)
10840.561 Million cell updates/sec

Title: US-10-024-806-1
Perfect score: 1326
Sequence: 1 gcgcggagcttccaagcccc.....aaaaaaaaaaaaaaaaaaaa 1326

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb.htg.*
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- 34: em.htg.pln.*
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- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	626.4	47.2	894	6	AX654380	AX654380 Sequence
2	489.2	36.9	1185	6	BN243085	AJ243085 Brassica
3	489.2	36.9	1186	6	A48348	A48348 Sequence 1
4	487.2	36.7	1159	6	A48349	A48349 Sequence 2
5	478.2	36.1	1124	8	BN243083	AJ243083 Brassica
6	472.4	35.6	1274	8	BN243084	AJ243084 Brassica
7	465	35.1	1276	8	CLCLR27	X64566 C.lanceolat
8	463.8	35.0	1065	8	AY081491	AY081491 Arabidops
9	463.8	35.0	1234	8	AF324985	AF324985 Arabidops
10	463.8	35.0	1357	8	AY059816	AY059816 Arabidops
11	459	34.6	1208	8	ATB08	X64464 A.thaliana
12	450.6	34.0	927	8	BN243086	AJ243086 Brassica
13	279.4	21.1	343550	1	AP003587	AP003587 Nostoc sp
14	272.2	20.5	11845	1	AE013105	AE013105 Thermoana
15	263.4	19.9	132419	1	D90907	D90907 Synecocyst
16	262.2	19.8	301200	1	AP05374	AP003374 Thermosyn
17	257.8	19.4	2678	1	BSU59433	U59433 Bacillus su
18	256.2	19.3	208780	1	BSUB0009	Z99112 Bacillus su
19	255.4	19.3	450	8	BNB08	X64463 B.napus mRN
20	254.4	19.2	747	6	E65145	E65145 Process for
21	248.4	18.7	347050	1	AL591981	AL591981 Listeria
22	248.4	18.7	349980	6	AX641670	AX641670 Sequence
23	247.2	18.6	303249	1	AP001515	AP001515 Bacillus
24	246.8	18.6	300150	1	AP004598	AP004598 Oceanobac
25	246.8	18.6	302481	1	AE017010	AE017010 Bacillus
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33	236.2	17.8	738	6	AX621928	AX621928 Sequence
34	236.2	17.8	929	6	AX583740	AX583740 Sequence
35	236	17.8	298050	1	AP003189	AP003189 Sequence
36	232.4	17.5	313450	1	AL596170	AL596170 Listeria
37	232.4	17.5	319630	6	AX413016	AX413016 Sequence
38	232.4	17.5	349980	6	AX417046	AX417046 Sequence
39	231.6	17.5	13165	1	AE007854	AE007854 Clostridi
40	221.4	16.7	771	1	AY142784	AY142784 Heliodaci
41	219.4	16.5	290117	1	AE017028	AE017028 Bacillus
42	218.2	16.5	300029	1	AE015936	AE015936 Clostridi
43	217.2	16.4	11523	1	AF197933	AF197933 Streptoco
44	217.2	16.4	12039	1	AE007354	AE007354 Streptoco
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ALIGNMENTS

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LOCUS	AX654380					
DEFINITION	AX654380					
ACCESSION	AX654380					
VERSION	AX654380.1	GI:29157194				
KEYWORDS	Oryza sativa					
SOURCE	Oryza sativa					
ORGANISM	Oryza sativa					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.					
AUTHORS	Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.					

TITLE	Plant genes involved in defense against pathogens
JOURNAL	Patent: WO 0300898-A 4250 03-JAN-2003; Syngenta Participations AG (CH)
FEATURES	Location/Qualifiers
source	1..894
BASE COUNT	251 a 164 c 250 g 227 t 2 others
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Best Local Similarity	87.2%; Pred. No. 1.8e-117; Indels 0; Gaps 0;
Matches 687; Conservative 0; Mismatches 101;	
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Qy	445 AAGACGAGTGCAGAGTTCCTGGTAAACTATGTCGCGGTCTTCGAAAGAGGCTGAAGAGTGC 504
Db	226 AAGCTGGGTGCAAGTCTCTGGTGAATCTATGCCCCGATCCTCAAAGAGGCTGAAGAGTGC 285
Qy	505 TCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATCACTTCGGGAGAGATGTTTCAAAA 564
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Qy	565 GAAGCTGATGTAGAGTCTATGATGAAGACGAGCTCTAGATAAATGGGGAAACAATAGATGTG 624
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Qy	625 CTGCTAATAATGCAGAGATTTACACGACACACATTTGTTGATGAGATGAAGAATCTCAG 684
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Qy	685 TGGCAAGACGTAATGTACTGAACTTTACTGGCGTCTTCCTTTGTACACAGGCTGCAACA 744
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Qy	745 AAGCTAATGATGAAGAGAGAAAGGGAATAATCAACTTGCATCTGTAGTGTGCTTT 804
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Qy	805 ACTGGCAATGTTGGCCACGCTAAATATAGCCGACGAGGCTCGAGGTGATTTGTTTCA 864
Db	586 GTTGTGTAATTTGGCCAACTAATTAACAGTCTGCCAAGGCTGGGTTATTGGTTTCA 645
Qy	865 AAAACAGTTGCCAGGAGTATGCACGACGAATATCAATGTGATGCTATTTGCACAGGG 924
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Qy	1045 GCCCTTAACCCCGCAGCTAGCTATATGATCTGACAGAGGTGCTTCAATTTACGCGAGGATG 1104
Db	826 GCTCTCAATCTCTGCGCCAACTAATCAATCAGGGAAGGTTCTTCAATCATGATGAGGATG 885
Qy	1105 GTAATGTA 1112
Db	886 GTGATGTA 893

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Db 384 GTCAGCAAGAGGCTGAGGAAGTCTTCAACAGAGATTGAAGCATATGGAGGCGAGGCTAT 443
Qy 540 CACCTTCGGAGAGATGTTTCAAAAGAGAGCTGATGTAGAGTCTATGATGAAGAGAGCTCT 599
Db 444 TACTTTTGGGGTGATGCTCTCAAGAGGCTGATGTGAGGATGATGAAGCAACGCTAT 503
Qy 600 AGATAAATGGGAAACATAGATGTGCTGTGTAATAATGACGGATTAACAGAGACACATT 659
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Qy 660 GTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAATTGATCTGAATCTTACGGCT 719
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Qy 1080 GGCTCTTACATTCACGAGGAGGATGATTAATGATGATTTGATTTAG 1125
Db 984 GGCAATCACCATTGATGAGGATTTGCCATCTAGCATTTGTTAAG 1029

RESULT 3
A48348
LOCUS 1186 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 1 from Patent WO9602652.
ACCESSION A48348
VERSION A48348.1 GI:2302139
KEYWORDS
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1. (bases 1 to 1186)
Slabas,A.R., White,A., Chase,D., Elborough,K. and Fentem,P.A.
beta -KETOACYL ACP REDUCTASE GENES FROM BRASSICA NAPUS
Patent: WO 9602652-A 1 01-FEB-1996;
ZENECA LTD (GB)
Other publication AU 2933695 960216.
FEATURES
Location/Qualifiers
1..1186
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BASE COUNT 317 a 256 c 304 g 309 t
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ORIGIN

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Best Local Similarity 69.2%; Pred. No. 1.9e-89;
Matches 696; Conservative 0; Mismatches 308; Indels 2; Gaps 2;
Qy 121 CTCCTCTTCGGCTCTTGGCTCCGAGCGCCCTCTATGGCCACGCGCGCCGACCGCA 180
Db 26 CTCCTCTCTCCCTCTCCACCCGCTCTCACCTCTCTCTCCGTTGATGGCAACACCGTC 85
Qy 181 GCAGCAGCAGCAGCTCTCTCCCGCTGCGGTGGAGCAGCGCGCGCGCGCGCTCC 240
Db 86 GCAGCAACAAGCTCACTCTTGAAGC-CGTCAAGAGCTCGGTTTCCGTGAGATCG 144
Qy 241 CGCCGGGGTTCGTCACTGTTGGTGGAGCGCCCGCTTCTCTCCCA-CGCTGCGGTC 299
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Qy 300 CGGCGGTGGGTTCTCTGGTGTGAAACCCATGTTGCTGCTTTGAAACAGAGTTGTA 359
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Qy 360 AGATGCTACCAAGCTGGAAGCTCCAGTGTGTTGTTTACAGGTGCATCTAGAGGATGG 419
Db 265 AGCTGTTCCGAAAGTGAAGTCTCCGTTGGTCTGTTGCTGCTGCTTCCGAGAGGATGG 324
Qy 420 TAAGCAACTGCTCTAGCCCTTGGAAAAGCAGGATGCAAGGTTCTGTGTAACCTATGCCC 479
Db 325 TAAAGCTATTGCTCTTCTTGGGCAAGCTGGCTGCAAGGCTTTGTTGAACATGCTAG 384
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Qy 720 CTTCCTTTGTACACAGGCTGCAACAAAGTAAATGATGAAAGAAAGAAAGGAAATAT 779
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RESULT 4
LOCUS      A48349
DEFINITION Sequence 2 from Patent WO9602652.
ACCESSION  A48349
VERSION     A48349.1  GI:2302140
KEYWORDS   Brassica napus (rape)
SOURCE      Brassica napus (rape)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 1159)
AUTHORS     Slabas A.R., White A., Chase D., Elborough K. and Fentem, P.A.
TITLE        beta-KETOACYL ACP REDUCTASE GENES FROM BRASSICA NAPUS
JOURNAL      Patent: WO 9602652-A 2 01-FEB-1996;
              ZENECA LTD (GB)
COMMENT      Other publication AU 2933695 960216.
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Best Local Similarity 73.9%; Pred. No. 5e-89;
Matches 618; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 290 CGCTGCGGTCGCGCGCGTGGTCTCTGTTGTGTCACCAACCACCAATGCTCTGTTGTGAACAAG 349
Db 141 CGCGGCGAGTCATTCGCAACTCCACTGTTGTGAAGCTCAAGCGACAGCTGTTGACCAAT 200
QY 350 CAGTTGTAAAGATGCTACAGCTGGAAGCTCCAGTTGTTGTTGTTACAGGTGCACTGA 409
Db 201 CGACAGGGAAGCTGTTCCGGAAGTGGAGTCTCCGGTGTGCTGTTGACTGGTGTCTCGA 260
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QY 530 GTGAGGCTATCACTTCGGAGGAGATGTTTCAAAAGAGCTGATGTAGAGTCTATGATGA 589
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950 AACTTGGAGAGAGCTTGAGAGAAAATCTTGTCAACCATCCGTTAGGAGAGATATGCC 1009
801 AGCTTGGAGAGACATGGAGAAAATCTTGGGAACAATCCCATTTAGGACATATGAC 860
1010 AACGAGAGAGCTTGAGAGGTTGTCAGTCTCTGCGCTTAAACCCCGCAGCTAGCTATA 1069
861 AACCTGAGAGTGTGGCTGGCTTGGTAGAATTTTGGCTCTCAGTCTGAGCTGAGAGTATGA 920
1070 TGACTGAGAGGCTGTACAAATGACGAGGAGATGGTAATGTAAGATTTGAGTTAG 1125
921 TCACGAGACAGCAATTCACCAATGATGAGGATTTGCCATCTAGGCAATTTGTTAAG 976

RESULT 5
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LOCUS      Brassica napus partial mRNA for 3-oxyacyl-[acyl-carrier protein]
DEFINITION reductase, isoform 1 (bkrl gene).
ACCESSION  AJ243083
VERSION     AJ243083.1  GI:14422246
KEYWORDS   3-oxyacyl-[acyl-carrier protein] reductase; bkrl gene.
SOURCE      Brassica napus
ORGANISM    Brassica napus
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1
AUTHORS     McDonald, P.S., White, A.J., Elborough, K.M. and Slabas, A.R.
JOURNAL     Unpublished
            2 (bases 1 to 1124)
REFERENCE   McDonald, P.
AUTHORS     Direct Submission
TITLE        Submitted (10-JUN-1999) McDonald P., Department of Biological
JOURNAL     Sciences, University of Durham, Science laboratories, South Road,
            Durham, DH1 3LE, UNITED KINGDOM
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Query Match      36.1%; Score 478.2; DB 8; Length 1124;
Best Local Similarity 74.7%; Pred. No. 3.4e-87;
Matches 600; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

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 DEFINITION
 C.lanceolata mRNA for beta-ketoacyl-ACP reductase.
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 VERSION
 X64566.1 GI:18045
 KEYWORDS
 3-oxoacyl-[acyl-carrier protein] reductase; beta-ketoacyl-ACP reductase; CILKLR27 gene.
 SOURCE
 Cuphea lanceolata
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Lythraceae; Cuphea.
 REFERENCE
 1 Klein,B., Pawlowski,K., Horicke-Grandpierre,C., Schell,J. and Topfer,R.
 TITLE
 Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta-ketoacyl-ACP reductase
 JOURNAL
 Mol. Gen. Genet. 233 (1-2), 122-128 (1992)
 MEDLINE
 92293104
 PUBMED
 1376402
 REFERENCE
 2 (bases 1 to 1276)
 AUTHORS
 Toepfer,R.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (21-FEB-1992) R. Toepfer, MPI f Zuechtungsforschung, Carl-von-Linne-Weg 10, 5000 Koeln 30, FRG
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 VERSION AY081491.1 GI:20148324
 KEYWORDS FLI CDNA
 SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 1065)
 Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M.,
 Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H.,
 Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A.,
 Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K.,
 Sakano, H., Sakurai, T., Satou, M., Seki, M., Shim, P., Yamada, K.,
 Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
 Direct Submission

TITLE Submitted (27-FEB-2002) DNA Sequencing and Technology Center,
 JOURNAL Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA

COMMENT comment 'e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN
 Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Nguyen, M.,
 Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J.,
 Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K.,
 Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shim, P.,
 Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.

Nguyen, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed
 equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.
 (SSP/Stanford) contributed equally to this work as PIs.

FEATURES

Location/Qualifiers

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CDS

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 VERSION AF324985.2 GI:13358177
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 Best Local Similarity 73.2%; Pred. No. 2.9e-84;
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SOURCE
ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
AUTHORS

Shinn, P., Chao, Q., Brooks, S., Chen, H., Cheuk, R., Johnson-Hopson, C.,
Khan, S., Kim, C.J., Banh, J., Bowser, L., Chung, M.K., Goldsmith, A.D.,
Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X.,
Miranda, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H.,
Southwick, A., Toriumi, M., Yamada, K., Yu, G., Davis, R.W.,
Theologis, A. and Ecker, J.R.

TITLE
JOURNAL

Arabidopsis cDNA clones

REFERENCE
AUTHORS

Shinn, P., Chao, Q., Brooks, S., Chen, H., Cheuk, R., Johnson-Hopson, C.,
Khan, S., Kim, C.J., Banh, J., Bowser, L., Chung, M.K., Goldsmith, A.D.,
Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X.,
Miranda, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H.,
Southwick, A., Toriumi, M., Yamada, K., Yu, G., Davis, R.W.,
Theologis, A. and Ecker, J.R.

TITLE
JOURNAL

Submitted (30-NOV-2000) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA

REFERENCE
AUTHORS

Shinn, P., Chao, Q., Brooks, S., Chen, H., Cheuk, R., Johnson-Hopson, C.,
Khan, S., Kim, C.J., Banh, J., Bowser, L., Chung, M.K., Goldsmith, A.D.,
Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X.,
Miranda, M., Nguyen, M., Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H.,
Southwick, A., Toriumi, M., Yamada, K., Yu, G., Davis, R.W.,
Theologis, A. and Ecker, J.R.

TITLE
JOURNAL

Submitted (16-MAR-2001) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA

COMMENT

On Mar 16, 2001 this sequence version replaced gi:11762117.
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H.,
Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Tracy, S.E., Banh, J.,
Bowser, L., Chung, M.K., Goldsmith, A.D., Jones, T., Karlin-Neumann, G.,
Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M.,
Palm, C.J., Pham, P.K., Quach, H.L., Sakano, H., Southwick, A.,
Tang, C.C., Toriumi, M., Yamada, K., Yu, G., Davis, R.W., Theologis, A.,
and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
contributed equally to this work as PIs.

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Matches 594; Conservative 0; Mismatches 217; Indels 0; Gaps 0;
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MACRILLOSOBI, K. W.
Molecular cloning of higher-plant 3-oxoacyl-(acyl carrier protein)-reductase. Sequence identities with the nodG-gene product of the

nitrogen-fixing soil bacterium Rhizobium meliloti
 Biochem. J. 283 (Pt 2), 321-326 (1992)
 JOURNAL 92246853
 MEDLINE 1575676
 PUBMED
 REFERENCE 2 (bases 1 to 1208)
 AUTHORS Mackintosh, R.W.
 TITLE Direct Submission
 JOURNAL Submitted (17-FEB-1992) R.W. Mackintosh, Dept of Biochemistry, Univ
 of Dundee, Dundee DD1 4HN, UK

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 QY 492 GCGTGAAGAGCTTCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATCATCCTTCGAGG 551
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 QY 612 AACATAGATGTGCTGTGTAATATGAGGAGTTATACAGAGACACATTTGTGATGAGGAT 671
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 Db 779 TATTTGTTTCCGAGACTCCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 946

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RESULT 12

ENA243086
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 DEFINITION
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 reductase, isoform 4 (bkr4 gene).
 ACCESSION
 AJ243086
 VERSION
 AJ243086.1 GI:14422252
 KEYWORDS
 3-oxoacyl-[acyl carrier protein] reductase; bkr4 gene.
 SOURCE
 Brassica napus
 ORGANISM
 Brassica napus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1
 McDonald, F.S., White, A.J., Elborough, K.M. and Slabas, A.R.
 AUTHORS
 Unpublished
 JOURNAL
 REFERENCE
 2 (bases 1 to 927)
 McDonald, F.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (10-JUN-1999) McDonald F., Department of Biological
 Sciences, University of Durham, Science laboratories, South Road,
 Durham, DH1 3LE, UNITED KINGDOM

FEATURES

Location/Qualifiers
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gene

BASE COUNT 284 a 157 c 237 g 249 t

CDS

Query Match 34.0%; Score 450.6; DB 8; Length 927;
 Best Local Similarity 75.0%; Pred. No. 1.4e-81;
 Matches 580; Conservative 0; Mismatches 184; Indels 9; Gaps 1;

BASE COUNT

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Qy	1008	CCAAACGAGGAAGTTGCAGGGTTGGTCEAGTTCCTGGCCCTTAACCCCGCAGCTAGCTA	1067
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RESULT 13									
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DEFINITION	Nostoc sp.	ECC 7120 DNA,	complete genome,	section 7/19.					
ACCESSION	AP003587	BA000019							
VERSION	AP003587.1	GI:17130808							

SOURCE	Nostoc sp. PCC 7120
ORGANISM	Nostoc sp. PCC 7120
	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
REFERENCE	1
AUTHORS	Kaneko, T., Nakamura, Y., Wolk, C.P., Kuritz, T., Sasamoto, S., Watanabe, A., Iriguchi, M., Ishikawa, A., Kawashima, K., Kimura, Kishida, Y., Kohara, M., Matsumoto, M., Matsuno, A., Muraki, A., Nakazaki, N., Shimpo, S., Sugimoto, M., Takazawa, M., Yamada, M., Yasuda, M. and Tabata, S.
TITLE	Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120
JOURNAL	DNA Res. 8 (5), 205-213 (2001)
MEDLINE	21595285
PUBMED	11759840
REFERENCE	2 (bases 1 to 343550)
AUTHORS	Kaneko, T.

TITLE
JOURNAL

Direct Submission
Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research, Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail: kaneko@kazusa.or.jp,
URL: http://www.kazusa.or.jp/cyanobase/,
Tel: 81-438-52-3935 (ex.2338), Fax: 81-438-52-3934)
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Qy 438 CCTTGGAAAGCAGGATGCAAGGTTCTGTTAACTATGCCGCTCTCCAAAGAGGCTCA 497
Db 194064 ATTAGCTAATATGTTGCTACTGTTAGTGGTCAATAGCTAGTCTTAGCACTGCTGCCGA 194123
Qy 498 AGAGGTCTCCAAAGAGATTGAAGCATCTGTTGGTGGAGGCTATCACCTTCGAGGAGATGT 557
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RESULT 14
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 DEFINITION Thermoanaerobacter tengcongensis strain MB4T, section 132 of 244 of the complete genome.
 ACCESSION AE013105 AE008691
 VERSION AE013105.1 GI:20516482
 KEYWORDS
 SOURCE Thermoanaerobacter tengcongensis
 ORGANISM Thermoanaerobacter tengcongensis
 Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 Thermoanaerobacteriaceae; Thermoanaerobacter.

REFERENCE
 AUTHORS Bao, Q., Tian, Y., Li, W., Xu, Z., Xuan, J., Hu, S., Dong, W., Yang, J., Chen, Y., Xue, Y., Xu, Y., Lai, X., Huang, L., Dong, X., Ma, Y., Ling, L., Tan, H., Chen, R., Wang, J., Yu, J. and Yang, H.
 TITLE A Complete Sequence of the T. tengcongensis Genome
 JOURNAL Genome Res. 12 (5), 689-700 (2002)
 MEDLINE 21992816
 PUBMED 11997336

REFERENCE
 AUTHORS Bao, Q., Xu, Z., Hu, S., Dong, W., Chen, Y., Wang, J., Yu, J. and Yang, H.
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-2001) Beijing Genomics Institute/Genomics and Bioinformatics Center, Institute of Genetics and Development, Chinese Academy of Sciences, Beijing Airport Industrial Zone B6, Beijing 101300, China
 3 (bases 1 to 11845)
 Li, W., Xuan, J., Yang, J., Ling, L. and Chen, R.
 Direct Submission
 Submitted (07-OCT-2001) Institute of Biophysics, Chinese Academy of Sciences, Beijing 100101, China
 4 (bases 1 to 11845)

REFERENCE
 AUTHORS Tian, J., Xue, Y., Xu, Y., Lai, X., Huang, L., Dong, X., Ma, Y. and Tan, H.
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 JOURNAL Submitted (07-OCT-2001) Institute of Microbiology, Chinese Academy of Sciences, Beijing 100080, China
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terminator

gene

CDS

misc_feature

misc_feature

RBS

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misc_feature

RBS

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gi|7433733|pir||H9620 [acyl-carrier-protein]
S-malonyltransferase (EC 2.3.1.39) fabd [validated] -
Bacillus subtilis gi|2337819|emb|CAA74249.1| (Y13937)
putative FabD protein [Bacillus subtilis]
gi|2633962|emb|CAB13463.1| (Z99112) malonyl CoA-acyl

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carrier protein transacylase [Bacillus subtilis], score
20.5%; Score 272.2; DB 1; Length 11845;
Best Local Similarity 61.7%; Pred. No. 5.8e-45;
Matches 452; Conservative 0; Mismatches 278; Indels 3; Gaps 1;
QY 385 GTTGTGTTGTTCACAGGAGGTTCTAGAGGATGTTGTAAGCAACTGCTTACCCCTTGA 444
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DB 4072 AAAGATGGCTTTAAATTTGCTATTAATTTGTAAGGACGATAGAGTGCAGAGAGATT 4013
QY 505 TCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATCACTTCGGAGGAGATGTTTCAAAA 564
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QY 565 GAAGCTGATGATGATCTATGATGAAGCAGCTCTAGATAAATGGGGAACATAGATGTC 624
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QY 1105 GTAATCTAAGATT 1117
DB 3415 GTTATGTAATATT 3403
RESULT 15
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LOCUS
DEFINITION
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D90907.1
GI:1652618
D90907
SYNCHOCYSTIS SP. PCC 6803
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Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
REFERENCE
1
Kaneke, T., Tanaka, A., Sato, S., Kotani, H., Suzuki, T., Miyajima, N.,
Sugliura, M. and Tabata, S.

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Query Match 19.9%; Score 263.4; DB 1; Length 132419;
 Best Local Similarity 59.7%; Pred. No. 5.5e-43;
 Matches 466; Conservative 0; Mismatches 306; Indels 9; Gaps 1;
 Qy 331 GTTGCTGCTGTGAACAGCAGTGTGTAAGAGATGCTACCAAGCTGGAAGCTCCAGTTGTT 390
 Db 96050 GCTGCTGATTACGTCCTTATAGGAGAACAGTTTATGACGGCATTAAACGGCACAGTGGCA 96109
 Qy 391 GTTCTTACAGTGCATCTAGAGGATGGTAAGCACTGCTTAGCCCTTGGAAAAGCA 450
 Db 96110 TTGTAACGGGGGCATCCCGGGGTAITGGTAAAGCGACGGCTTTGGCCCTGGCCGCCACG 96169
 Qy 451 GGATGCAAGGTTCTGGTAAACTATGCCCGGTCCTCGAAAGAGGCTGAAGAGTCTCCAAA 510
 Db 96170 GGCAATGAAGTGTAGTAGTAATGCTCAATCCAGTACGGCCGCCGATGCTGTGGTAGCG 96229
 Qy 511 GAGATTGAAGCATCTGGTGTGAGGCTATCACTTCGGAGGAGATGTTTCAAAAAGAGCT 570
 Db 96230 GAAATTATTCCAAACGGGGGAGAGCGGATCCCGTGCAGGCCAATGTGGCTAATGCTGAC 96289
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 Db 96470 ATGCTCAAGCAAAAAAGTGGCGGTATCATTAACATCACTTCTGTAGCGGGCATATGGGG 96529
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Search completed: November 7, 2003, 14:49:07
 Job time : 5011 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 13:13:59 ; Search time 398 Seconds

(without alignments)
8993.605 Million cell updates/sec

Title: US-10-024-806-1

Perfect score: 1326

Sequence: 1 gcgggagcttcacagcc.....aaaaaaaaaaaaaaaaaa 1326

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 13Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	490.8	37.0	1185	17	AAQ99304 Rape seed beta-ket
2	488.8	36.9	1155	17	AAQ99305 Rape leaf beta-ket
3	403.4	30.4	1053	21	AAAC4588 Arabidopsis thalia
4	345.4	26.0	822	21	AAAC4385 Arabidopsis thalia
5	254.4	19.2	747	21	AAZ45749 Nucleotide sequenc
6	248.4	18.7	294528	24	ABA03041 Listeria monocytog
7	239.8	18.1	6251	18	AAV74336 Staphylococcus aur
8	238	17.9	741	23	AA554388 Staphylococcus aur

9	237.4	17.9	741	21	AAA74685 Staphylococcus aur
10	237.4	17.9	741	22	AAD06206 S. aureus NADPH-de
11	237.4	17.9	741	23	AA55068 Staphylococcus aur
12	237.4	17.9	741	23	AA55365 Staphylococcus aur
13	236.8	17.9	738	23	AA551824 Staphylococcus aur
14	236.2	17.8	929	25	ABT14915 Pathogen specific
15	232.4	17.5	319630	24	ABQ67194 Listeria innocua c
16	232.4	17.5	3011208	24	ABQ69245 Listeria innocua D
17	217.2	16.4	19702	19	AAV52140 Streptococcus pneu
18	217.2	16.4	2162598	25	AB556454 Streptococcus pneu
19	215	16.2	729	25	ABX08055 S. pneumoniae type
20	215	16.2	750	24	ABN92525 Staphylococcus epi
21	214	16.1	3649	22	AAH54361 S. epidermidis gen
22	212.8	16.0	744	24	ABK73267 Bacillus clausii g
23	212.8	16.0	3580	19	AAV65243 S. pneumoniae gene
24	212.2	16.0	2365589	24	ABA90521 Genomic sequence o
25	211.8	16.0	732	21	AAA74684 Streptococcus pneu
26	211.8	16.0	732	22	AAH90731 CFE 35 coding sequ
27	211.8	16.0	732	23	AA553625 Streptococcus pneu
28	211.8	16.0	756	22	AAH90844 2CFE 35 coding seq
29	210.2	15.9	732	23	AA555846 Streptococcus pneu
30	184.4	13.9	1196	19	AAAT98542 DNA encoding a S.
31	183	13.8	732	24	ABN67976 Streptococcus poly
32	179	13.5	7916	21	AAAS0142 Bacillus megaterium
33	176.6	13.3	1209	19	AAV37406 Streptococcus pneu
34	174.2	13.1	732	24	ABN68642 Streptococcus poly
35	174.2	13.1	2155561	24	ABN71527 Streptococcus poly
36	173	13.0	6021	20	AAAX13395 Enterococcus faeca
37	173	13.0	6021	24	AB599190 Enterococcus faeca
38	171	12.9	537	24	ABK79246 Bacillus clausii g
39	166.6	12.6	738	23	AA553187 Enterococcus faeca
40	166.6	12.6	1199	18	AAK30801 Streptococcus pneu
41	158.8	12.0	468	24	ABK74996 Bacillus lichenifo
42	156.8	11.8	735	21	AAZ45746 Nucleotide sequenc
43	156.8	11.8	735	23	AA552392 E. coli DNA for ce
44	156.8	11.8	735	24	ABX17285 DNA encoding Poly3
45	153.2	11.6	1830121	17	AAAT4063 Haemophilus influe

ALIGNMENTS

RESULT 1

AAQ99304
ID AAQ99304 standard; cDNA to mRNA; 1185 BP.

XX AC AAQ99304;

XX AC

DT 13-APR-1996 (first entry)

XX Rape seed beta-ketoacyl-ACP-ketoreductase PJRS10.1 cDNA.

XX Rape; seed; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase;
KW plasmid PJRS10.1; cDNA library; embryo; Arabidopsis thaliana;
KW probe; hybridization; plasmid rescue; Escherichia coli;
KW poly-A tail; plasmid; stroma; transit peptide; vector; cassette;
KW antisense; oilseed; transgenic plant; crop improvement; lipid;
KW metabolic engineering; polymer; rapeseed oil; ss.

XX Brassica napus.

OS Brassica napus.

XX Key Location/Qualifiers

FT 5'UTR 1..69

FT transit_peptide 70..234

FT CDS /tag= a

FT /tag= b

FT /tag= c

FT /product= Beta-keto-acyl-ACP-ketoreductase

FT mat_peptide 235..1015

FT /tag= d

FT 3'UTR 1018..1185

FT /tag= e

XX	PD	XX	101-FEB-1996.	QY	770	GAATAATTATCAACATTCGATCTCTAGTGTGCTTACTGGCAATGTTGGCCAGCTAATT	829
XX	PF	XX	17-JUL-1995; 95WO-CB01678.	Db	617	GAAGATCATCAACATTCGGTCACTGTTGGTCTCATTTGGTAATATTGGCCAGCAAACT	676
XX	PR	XX	20-JUL-1994; 94GB-0014622.	QY	830	ATAGCGAGCCAGCGCTGGAGTATGTTGTTTCAAAAACAGTTGCCAGGGAGTATGCAA	889
XX	PA	XX	(ZONE) ZENECA LTD.	Db	677	ACGCTGCTGCTAAAGCTGGTCTTATTGGGTTCTCAAGACTGCCGCCAGAGAGGGTGCGA	736
XX	PI	XX	Chase D, Elborough K, Pentem PA, Slabas AR, White A;	QY	890	GCAGAAATATCAATGTGAATCTATTGCACAGGGTTCATTGTCATCTGATATGATGCCG	949
XX	DR	XX	WPI; 1996-105914/11.	Db	737	GCAGAAATATCAATGTCAATGTGTTGCTCCCTGGGTTCAATTCGATCTGACATGCTGCA	796
XX	DR	XX	P-PSDB; AAR89323.	QY	950	AACCTTGAGAAAGAGCTTGAGAAAGAAATCTTGTCAACCATTCGGTTAGGGAGATATGCC	1009
PT	PT	XX	New isolated rape beta-ketoreductase DNA - used to develop plants	Db	797	AGCTTGAGAAAGACATGGAAGAAATCTTGGGAAACAATCCCATAGGACGATATGGAC	856
XX	PT	XX	with lower or higher oil contents or with altered oil compsn.	QY	1010	AACGAGAGAAAGTTTCAGGGTTGTCGAGTTCTCTGGCCCTTAACCCCGCAGCTAGCTATA	1069
XX	PS	XX	Claim 2; Page 16; 29pp; English.	Db	857	AACCTGAAAGATGTGGCTGGCTTGGTAGAATTTCTTGGCTCTCAGTCTCGAGCTAGTTACA	916
XX	CC	XX	The sequence corresponds to a rape leaf beta-ketoreductase cDNA	QY	1070	TGACTTGGACAGTGTCTTACAATTGACGGAGGATGTTAATGTAAAGATTTGAGTTAG	1125
CC	CC	XX	clone (plasmid pJRL6.2 insert). The clone has been isolated by	Db	917	TCACAGGACAGCATTCACCATTTGATGGAGGATTGGCCATCTAGGCAATTTGTTAAG	972
CC	CC	XX	screening of a cDNA library, derived from rape mRNA, with an	RESULT 3			
CC	CC	XX	Arabidopsis thaliana beta-ketoreductase 0.96-kb cDNA probe,	AAc44588			
CC	CC	XX	subcloning in plasmid pSK and plasmid rescue in Escherichia coli	ID	AAC44588 standard; DNA; 1053 BP.		
CC	CC	XX	present. The DNA may be inserted in a vector or expression cassette	XX	AAC44588;		
CC	CC	XX	in sense or antisense orientation for expression in an oilseed	XX	18-OCT-2000 (first entry)		
CC	CC	XX	plant, e.g. for production of transgenic rape plants with low or	DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 43381.		
CC	CC	XX	modified oil content, diversion of metabolism to alternative storage	KW	Hybridisation assay; genetic mapping; gene expression control;		
CC	CC	XX	compounds, e.g. starch, protein or engineered polymers, or	KW	protein identification; signal transduction pathway;		
CC	CC	XX	production of plants with enhanced oil content. The DNA may also be	KW	metabolic pathway; promoter; termination sequence; ss.		
CC	CC	XX	used as a probe to obtain similar genes from other plants. The	OS	Arabidopsis thaliana.		
CC	CC	XX	transit peptide DNA may be used in gene fusions to direct other	XX	EP1033405-A2.		
CC	CC	XX	proteins to leaf plastids.	XX	06-SEP-2000.		
XX	SQ	XX	Sequence 1155 BP; 310 A; 230 C; 309 G; 306 T; 0 other;	PF	25-FEB-2000; 2000BP-0301439.		
			Query Match 36.9%; Score 488.8; DB 17; Length 1155;	PR	25-FEB-1999; 99US-0121825.		
			Best Local Similarity 74.0%; Pred. No. 7.2e-92;	PR	05-MAR-1999; 99US-0123180.		
			Matches 619; Conservative 0; Mismatches 217; Indels 0; Gaps 0;	PR	09-MAR-1999; 99US-0123548.		
QY	290	CGCTGCGGTCGGCGTGGTCTCTGTTGTCGAAACCCCATGTTGCTGTGTTGTAACAAG	349	PR	23-MAR-1999; 99US-0125788.		
Db	137	CGCGGCACTATTGCGAACCTCCACTGTGTGAAGCTCAAGCGACAGCTGTGTGAGCAAT	196	PR	23-MAR-1999; 99US-0126264.		
QY	350	CAGTTGTAAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACAGGTGCATCTA	409	PR	29-MAR-1999; 99US-0126785.		
Db	197	CGACAGGAGAGCTGTTCCGAACTGGAGTCTCCGGTGGTGTGTTGACTGGTCTTGA	256	PR	01-APR-1999; 99US-0127462.		
QY	410	GAGGATTTGTTAAGCAACTGCTCTAGCCCTTGAAAGACGAGTGAAGTTCTGTAA	469	PR	06-APR-1999; 99US-0128234.		
Db	257	GAGGATTTGTTAAGCTATTGCTCTTTCTTTGGGCAAGCTGGCTGCAAGGTCTTGGTGA	316	PR	08-APR-1999; 99US-0128714.		
QY	470	ACTATGCCGCTCTCGAAGAGCTGAAGAGTCTCCAAAGAGATTGAAGCATCTGGTG	529	PR	16-APR-1999; 99US-0129845.		
Db	317	ACTATGCTAGTCAAGAGAGGCTGAGGAAGTTTCTAAACAGATTGAACATATGGAG	376	PR	21-APR-1999; 99US-0130077.		
QY	530	GTGAGGCTATCACCTTCGGAGGAGATTGTTCAAAGAGAGCTGATCTAGTCTATGATGA	589	PR	23-APR-1999; 99US-0130449.		
Db	377	CCAGGCTATTACTTTTGGGGGTGATGCTCCAAAGAGGCTGATGTGGAAGCCATGATGA	436	PR	23-APR-1999; 99US-0130510.		
QY	590	AAGCAGCTCTAGATAAAATGGGAAACAATAGATGCTGCTGTAATATTCAGGATATCAC	649	PR	28-APR-1999; 99US-0131449.		
Db	437	AAACCGCTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	496	PR	30-APR-1999; 99US-0132048.		
QY	650	GAGACACATTTGTTGATGAGTGAAGAAATCTCAGTGGCAGACGCTAATTCATCTGAATC	709	PR	04-MAY-1999; 99US-0132484.		
Db	497	GCGATACCTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	556	PR	05-MAY-1999; 99US-0132485.		
QY	710	TTACTGGGCTCTCTCTTTGTACACAGGCTGCAACAAAAGTATGATGATGATGATGATG	769	PR	06-MAY-1999; 99US-0132487.		
Db	557	TCACTGGAGTCTTTCTCTGTATCCCGAGCGAACCAAGATCATGATGATGATGATGATG	616	PR	07-MAY-1999; 99US-0132863.		

PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
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PR 18-JUN-1999; 99US-0139460.
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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
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PR 08-JUL-1999; 99US-0142803.
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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
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PR 27-JUL-1999; 99US-0145919.
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PR 03-AUG-1999; 99US-0147038.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 10-SEP-1999; 99US-0153070.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.

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PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	26-OCT-1999;	99US-0161920.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.

QY 552 AGATGTTTCAAAAGAGCTGATGAGTCTATGATGAAGCGCTCTAGATAATGGG 611
 Db 399 TGATGTTCTCGAAAGCAGCTGATGATGATGATGAAGCGCTCTAGATAATGGG 458
 QY 612 AACATAGATGCTGCTGTAATAATACAGGATTTACAGGAGACACATTTGATGAGGAT 671
 Db 459 AACCATGATGTTGTTTAAACATGAGGAATTTACGGATACCTGTTTATACGAAT 518
 QY 672 GAAGAAATCTAGTGGCAAGCTAAATGATCTGAATCTTACTGCGCTCTTCTTTGTAC 731
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 QY 732 ACAGGCTCAACAAAGATGATGATGAAGAGAGGAGAAATTTATCAATTCATC 791
 Db 579 TC-----AGGGAAGAAATCATCAATATCTCGTC 605
 QY 792 TGTAGTTGTTCTTACTGCGCAATTTGGCCAAAGCTAATTTATAGCGCAGCCAGGCTGAGT 851
 Db 606 AGTTGTTGTTCTCTTGTGTAATTTGTTGTAAGCAAACTACGACGCGCTTAAGTGGAT 665
 QY 852 GATTGTTTCAAAAACAGTTCGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGC 911
 Db 666 TATTTGCTTTCCAGACTGCTGCCAGAGAGGTTGGCGAGCAGGAATATAAATGTCATGT 725
 QY 912 TATTGACACAGGTTTCAATGCTATCTGATGATGATGCTGCGAACTTGGAGAGAGCTTGAGAA 971
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 QY 972 GAAATCTTGTCAACCATTCGTTAGG 998
 Db 786 GAAATCTTGGGACAAATCCCATTAGG 812

RESULT 5

AAZ45749
 ID AAZ45749 standard; DNA; 747 BP.
 XX AAZ45749;
 AC AAZ45749;
 XX
 DT 06-APR-2000 (first entry)
 DE Nucleotide sequence of a fabG (beta-ketoacyl-ACP reductase) gene.
 XX Beta-ketoacyl-ACP reductase; Type II fatty acid synthetase;
 KW stereoselectivity; 4-chloroacetoacetic acid ester;
 KW (S)-4-halo-3-hydroxybutyric acid ester; 4-halo-acetoacetic acid ester;
 KW beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductase;
 KW polybeta-hydroxy fatty acid biosynthesis; optically active;
 KW 4-halo-3-hydroxybutyric acid ester; ss.
 XX
 CS Bacillus subtilis.

XX Key Location/Qualifiers
 FH 1..747
 FT CDS /*tag= a
 FT /product= "beta-ketoacyl-ACP reductase"

XX EF955375-A2.

XX 10-NOV-1999.

XX 10-MAY-1999; 99EP-0109403.

XX 08-MAY-1998; 98JP-0126507.

PR 21-OCT-1998; 98JP-0300178.

PR 05-APR-1999; 99JP-0098205.

XX (DAIL) DAICEL CHEM IND LTD.

XX Yamamoto H;

XX WPI; 2000-118183/11.

DR P-PSDB; AAY54422.

XX Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester -

PS Example 7; Page 20-21; 34pp; English.

XX The present sequence encodes a beta-ketoacyl-ACP reductase protein of *Bacillus subtilis*. The beta-ketoacyl-ACP reductase enzyme constitutes a type II fatty acid synthetase. The enzyme has an extremely high reducing activity and stereoselectivity towards 4-chloroacetoacetic acid ester. The specification describes a method for producing a (S)-4-halo-3-hydroxybutyric acid ester. The method comprises asymmetrically reducing 4-halo-acetoacetic acid ester or its derivative with beta-ketoacyl-acyl carrier protein reductase constituting type II fatty acid synthase, or acetoacetyl-CoA reductase constituting the polybeta-hydroxy fatty acid biosynthesis system. The novel method is used to produce optically active 4-halo-3-hydroxybutyric acid ester, with a high purity.

XX Sequence 747 BP; 243 A; 155 C; 175 G; 174 T; 0 other;

Query Match 19.2%; Score 254.4; DB 21; Length 747;

Best Local Similarity 59.8%; Pred. No. 2.5e-43;

Matches 445; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 370 ABCTGGAGCTCCAGTTGTTGTTACAGCTGCATCTAGAGGATTTGTAAGCAACT 429

Db 7 ATGCTTAATGATAAAGCGCTATTGTCACCTGGCATCCCGGGAATCCGCGCTCAATC 66

QY 430 GCTCTAGCCCTTGGAAAAGCAGGATGCAAGTTCCTGGTAAACTATGCCCGTCTCGAAA 489

Db 67 GCCTTGCTCTGCAAAAAGCGGAGCAATGTTGCTGAACTACTCCGCAATGAAGCG 126

QY 490 GAGGCTGAAGAGGTTCTCAAAGAGATTGAAGCATCTGGTGGTGAAGCTATCACTTCGGA 549

Db 127 AAAGCAATGAAGTGTGATGAAATCAATCAATGGGAGAGAAACAATTTGCTGTAATA 186

QY 550 GGAGATGTTTCAAAGAGCTGATGTAGAGTCTATGATGAAAGAGCTCTAGATAATGG 609

Db 187 GCGATGTAATCAATCCCGAAGATGTAACAAATGATAAAGAAACATTTGCTGTTTT 246

QY 610 GGAACAATAGATGTGCTGTAATAATATGAGGATTTACAGACACATTTGTTGATGAGG 669

Db 247 TCTACGATTGACATCTCTGTTAATAATGCGGAAATTTACAAGAGACAATCTCATGAGA 306

QY 670 ATGAAGAAATCTCAGTGGCAAGCGTAATTGATGTAATCTTACTGGGCTTTCCTTTGT 729

Db 307 ATGAAGAAAGACGAATGGGATGACGCTATTAAACATTAACCTGAAGGTTGTTTCAACTGC 366

QY 730 ACACAGGCTGCAACAAAGTAAATGATGAAAAAGAGAAAGGAAAAATTTATCAATTGCA 789

Db 367 ACAAAGCTGTTACAGACAAATGATAAGAGCTTCAGCGCGCAATTTAAGCTATCG 426

QY 790 TCTGTAGTTGGTCTTACTGCGCAATGTTGCCAAGCTAATTTATAGCCAGCGAGGCTGGA 849

Db 427 TCTATGTCGCGCTCAGCGGAAACCCCTGACAAAGCAACTACGTGCTGCAAAAGCGGC 486

QY 850 GTGATTTGTTTCAAAAACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAAT 909

Db 487 GTCATCGTTTAAACCAATCTTCTGCTAAAGAGCTCCGACGCGGAATATTACGGTAAAC 546

QY 910 GCTATTGCAACAGGTTTCAATGTCATCTGATATGACCTGCCGAATCTTGAGAGAGCTTGAG 969

Db 547 GCATAGCCCGAGGATTTATCTCACTGATATGACAGATAAATCTGCAAAAGAGCTTCAA 606

QY 970 AAGAAAAATCTTGTCAACCAATTCGTTAGGAGATATGGCCAAACAGAGAGGTTGAGGG 1029

Db 607 GACGAAATCTGAAACAAATTCGCTCGCGCTTTGGTGAACCTAGCGATGTCAGAGT 666

QY 1030 TTGGTCGAGTTCTCGGCCCTTAACCCCGCAGCTAGCTATATGACTGGAGAGGTTTACA 1089

Db 667 GTTGTCACTGCTTAGC---TTACAGAGGAGGCTCGTTATATGACAGGCGCAACGCTTCAT 723

PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR P-PSDB; AAU36529.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Claim 27; Seq ID No 8025; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 741 BP; 263 A; 106 C; 165 G; 207 T; 0 other;
SQ
Query Match 17.9%; Score 238; DB 23; Length 741;
Best Local Similarity 59.0%; Pred. No. 6.3e-40;
Matches 428; Conservative 0; Mismatches 295; Indels 3; Gaps 1;
388 GTTCTGTTACAGGTGATCTAGAGGATTCGTAAGGCACTGCTTAGCCCTTGGAAA 447
19 GCTTTAGTAACAGGTGCATCAAGAGAAATTGACGTAGTATTGCTTACAATTAGCAGAA 78
448 GCAGGATCAAGGTTCTGTTAACTATATCCCGGTCCTCGAAGAGGCTGAAGAGTCTCC 507
79 GAAGATATATGTAGCAGTAATATCTATCAGGACAGCAAGAAAGCTGAAGCAGTAGTC 138
508 AAAGAGATTGAAGCATCTGGTGGTGGAGGCTATCACCTTCGGAGGAGATGTTCAAAAGAA 567
139 GAAGAAATCAAGCTAAAGGTTTGCACAGTTTTCGATTCAAGCAATGTTGCCGATGCT 198
568 GCTGATGTAGTCTTATGATGAAGCAGCTCTAGATAATGGGAACAATAGATGCTGTG 627
199 GATGAAGTTAAGCAATGATTAAGAGTAGTAGCCAAATTTGGTCTTTAGATGTTTAA 258
628 GTAAATAATGCAAGGATTACAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGG 687
259 GTAAATAATGCAAGTATTACTCGCGATAATTTATTAAATGCGTATGAAGAACAGAGTGG 318
688 CAAGACGTAATGATGTAATCTTACTGGCGTCTTCCTTTGTACACAGGCTCCACAAAA 747
319 GACGATGTTATTGACACAACTTAAAGGTTGATTAACTGTATCCAAAAAGCAACACCA 378
748 GTAAATGCAAAAAAGAGAGAGGAAAAATATCAATGTCATCTGTAGTGGTCTTACT 807
379 CAAATGTTAAGCAACAGTAGTGGTGCTATCATCAATTTATCAAGTGTGTTGGACAGTA 438

808 GCAATGTTGGCAAGCTAATATATAGCGCAAGGCTGGAGTGTGTTTCAAAA 867
439 GGTAAATCCAGGACAAAGCAAACTATGTTGCAACAAAGCAGGTTGTTATTGTTTAACTAAA 498
868 ACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTAATGTAATGCTATTGACACAGGTTTC 927
499 TCTGGCGCGCGAATTAGCATCTCGTGTATCATCTGTAAATGCAAGTTCACCTGTTT 558
928 ATTGCATCTGATATGACTCCGAACTTTGAGAGAGAGCTTTGAGAAGAAAATCTTGTCAACC 987
559 ATTGTTTCTGATATGACAGATGCTTTAAGTGTAGCTTTAAGAGACAAATGTTGACTCAA 618
988 ATTCCGTTAGGAGATATGGCCAAACAGAGGAGTTGAGGGTTGTCAGTTCCTGGCC 1047
619 ATTCCGTTAGCAGGTTTGGTCAAGACACAGATATTGCTTAATACAGTAGCGTTCTTAGCA 678
1048 CTTAACCCTGCGAGTATGATGATGCTGACAGGCTTACAAATTCAGCGAGGAGTGTAA 1107
679 TCAGA---CAAGCAAAATATATTACGTTCAACAAATCATGTAATGTTGGAATGTAC 735
1108 ATGTAA 1113
736 ATGTAA 741
RESULT 9
AAA74685
ID AAA74685 standard; DNA; 741 BP.
AC AAA74685;
XX 07-DEC-2000 (first entry)
DT
DE Staphylococcus aureus fabG polynucleotide.
XX
XX Staphylococcus aureus; fabG; 3-ketoacyl-ACP reductase; antibacterial;
KW cytostatic; antiulcer; cancer; gastric ulcer; gastritis;
KW Helicobacter pylori infection; microbial infection; ds.
XX
XX Staphylococcus aureus.
Key Location/Qualifiers
CDS 1..741
FT /*tag= a
FT /product= "fabG polypeptide"
XX
XX WO200044773-A1.
XX
XX 03-AUG-2000.
XX
XX 19-JAN-2000; 2000WO-US01196.
XX
XX 28-JAN-1999; 99US-0238481.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Huang J, Mcdevitt D;
XX WPI; 2000-482968/42.
XX P-PSDB; AAB15707.
XX
XX FabG polypeptide, isolated from Staphylococcus aureus, is used to treat
PT microbial diseases, identify agonists and antagonists for treating
PT microbial infections and to detect diseases associated with microbial
PT infections -
XX
XX Claim 2; Page 2-3; 37pp; English.
XX
XX The present sequence encodes a fabG (3-ketoacyl-ACP reductase)
CC polypeptide from Staphylococcus aureus. A full length fabG gene was
CC isolated from an S. aureus WCUH 29 DNA library. fabG polynucleotides
CC and polypeptides are used for detection and treatment of microbial

CC diseases. They may also be used to identify antagonists and agonists
CC which can then be used to treat microbial diseases. Compounds that
CC interfere with the initial physical interaction between a pathogen and
CC a host have been identified. The compounds are able to prevent the
CC adhesion of bacteria to mammalian extracellular proteins in wounds,
CC prevent adhesion between mammalian extracellular proteins and
CC bacterial fabG proteins which mediate tissue damage and/or to block
CC normal progression of pathogenesis in infections mediated by
CC implantation of in-dwelling devices or other surgical techniques. The
CC fabG polypeptides, polynucleotides, antagonists and agonists are
CC especially useful in the treatment of *Helicobacter pylori* infection.
CC They may be used to decrease *H. pylori*-induced cancers and to prevent,
CC inhibit and/or cure gastric ulcers and gastritis.
XX
SQ Sequence 741 BP; 261 A; 105 C; 167 G; 208 T; 0 other;

Query Match 17.9%; Score 237.4; DB 21; Length 741;
Best Local Similarity 58.9%; Pred. No. 8.4e-40;
Matches 428; Conservative 0; Mismatches 236; Indels 3; Gaps 1;

QY 387 TGTGTTGTTACAGGTCATCTAGAGGATGGTGAAGCACTGCTTAGCCCTTGGAAA 446
Db 18 TGCTTTAGTAACAGGTCATCAAGAGGAATTTGACGTAGTATTGCGTTACAATTAGCAGA 77
QY 447 AGCAGGATGCAAGGTTCTGGTAACTATGCCGTCTCGAAGAGGCTGAAGGTCCTC 506
Db 78 AGAAGGATATAATGTACAGTAATACTATGACGGCGCAAGAGAACTGAAGCAGTAGT 137
QY 507 CAAAGAGATTGAAGCACTCGTGTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGA 566
Db 138 CGAAGAAATCAAGCTAAAGGTGTGACAGTTTTCGGATTCAGCAAAATGTCCGATGC 197
QY 567 AGCTGATGTAGTCTATGATGAAGCAGCTCTAGATAAATGCGGAAACAATAGATGTCT 626
Db 198 TGATGAAGTTAAAGCAATGATTAAGAAAGTAGTATTAGCCAAATTTGGTTCTTTAGATGCTT 257
QY 627 GGTAAATAATGCAGGATTTACACAGACACATTCGTGATGAGGATGAAGAAATCTCAGTG 686
Db 258 AGTAAATAATGCAGGATTTACTCCGGATAATTTATTAATGCTGTAAGAAAGAAAGAGTG 317
QY 687 GCAAGAGCTAATTCATCTGATCTTACTGGCGTCTTCTTTGTACACAGGCTGCAACAAA 746
Db 318 GGATGATGTTATTGACACAACTTAAGAGGTGTTATTAACTGTATCCAAAAGCAACACC 377
QY 747 AGTAATGATGAAGAAAGAGAGGAAATATCAATTCATCTGTAGTGTCTTTAC 806
Db 378 ACAAATGTTAAGACAACGTAGTGTGCTATCATCAATTTATCAAGTGTGTTGGAGCAGT 437
QY 807 TGCAATGTTGGCCAAAGCTAATTATAGCGCAGCAAGGCTGGAGTGTGTTTCACAA 866
Db 438 AGGTAAATCCGGACAGCAAACTATGTTGCAAAAGCAGGTGTTATGTTTAACTAA 497
QY 867 AACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGACAGGTT 926
Db 498 ATCTCGCGCGGTGAATTAGCATCTCGTGGTATCATCTGTAATGAGTTCACCTGGTT 557
QY 927 CATTCGATCTGATGATGCTGCGCACTTGGAGAGAGCTTGAAGAAATCTTGTCAAC 986
Db 558 TATTTGTTTCTGATATGACAGATGCTTTTAAGTGTATGAGCTTAAAGACAAATGTTGACTCA 617
QY 987 CATTCGTTAGGAGATATGCCAACAGAGGAAGTTTCAGGGTTGGTCGAGTTTCTGGC 1046
Db 618 AATTCGTTAGCAGTTTGTGTTCAAGACAGATATTTCTAATACAGTAGGTTCTTAGC 677
QY 1047 CCTTAACCCCGCAGTATGATGATGCTGAGCAGGTGCTTCAATTTGACGAGGAGTGGT 1106
Db 678 ATCAGA---CAAAGCAAAATATTTACAGGTCAACAACTCCATGTAATGTTGGTAATGTA 734
QY 1107 AATGTAA 1113
Db 735 CATGTAA 741

RESULT 10
AAD06206
ID AAD06206 standard; DNA; 741 BP.
XX
AC AAD06206;
XX
DT 31-JUL-2001 (first entry)
XX
DE S. aureus NADPH-dependent beta-ketoacyl-ACP reductase (FabG) DNA.
XX
KW FabG; high throughput method; fatty acid biosynthesis; therapy;
KW bacterial enzyme; biological agent screening; otitis media; empyema;
KW bacterial tracheitis; acute epiglottitis; thyroditis; lung abscess;
KW infective endocarditis; secretory diarrhoea; splenic; retroperitoneal;
KW intrarenal; perinephric; cerebral; cutaneous; abscess; blepharitis;
KW conjunctivitis; keratitis; endophthalmitis; preseptal; orbital;
KW cellulitis; dacryocystitis; epididymitis; abscess; toxic shock syndrome;
KW impetigo; folliculitis; wound infection; bacterial myositis;
KW septic arthritis; osteomyelitis; beta-ketoacyl-ACP reductase;
KW acyl carrier protein; ds.
XX
OS Staphylococcus aureus 'WCUH 29'.
XX
FH Key Location/Qualifiers
CDS 1..738
FT /tag= a
FT /product= "Staphylococcus aureus FabG"
XX
XX MO200130988-A1.
XX PN
XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000NO-US29451.
XX PR 27-OCT-1999; 99US-0161775.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PA (SMIK) SMITHKLINE BEECHAM PLC.
XX PI Dewolf W, Kallender H, Lonsdale JT;
XX WPI; 2001-316332/33.
XX P-PSDB; AAE02195.
XX High throughput method for screening for biological agents against
fatty acid biosynthesis comprises contacting a bacterial enzymatic
pathway with enzymes e.g. malonyl-CoA:ACP transacylase -
Example 16; Page 10; 94pp; English.
XX The present invention relates to a high throughput method for screening
biological agents affecting fatty acid biosynthesis, comprises
contacting a bacterial enzymatic pathway with enzymes. The method is
used for screening biological agents affecting fatty acid biosynthesis.
Agonists and antagonists of fab (fatty acid biosynthesis) are used to
inhibit, prevent or treat diseases such as infections of the upper
respiratory tract (e.g. otitis media, bacterial tracheitis, acute
epiglottitis, thyroiditis), lower respiratory (e.g. empyema, lung
abscess), cardiac (e.g. infective endocarditis), gastrointestinal (e.g.
secretory diarrhoea, splenic abscess, retroperitoneal abscess), central
nervous system (e.g. cerebral abscess), eye (e.g. blepharitis,
conjunctivitis, keratitis, endophthalmitis, preseptal and orbital
cellulitis, dacryocystitis), kidney and urinary tract (e.g.
epididymitis, intrarenal and perinephric abscess, toxic shock syndrome),
skin (e.g. impetigo, folliculitis, cutaneous abscess, cellulitis, wound
infection, bacterial myositis) and bone and joint (e.g. septic
arthritis, osteomyelitis).
XX The present sequence is a DNA encoding *Staphylococcus aureus* 'WCUH 29'
beta-ketoacyl-ACP (acyl carrier protein) reductase (FabG). In fatty
acid biosynthetic pathway, ketoester reduction is by FabG.
XX Sequence 741 BP; 260 A; 105 C; 168 G; 208 T; 0 other;
SQ

Db 318 GGATGATGTTATGACAACTTAAAGTGTTATTAAGTCTGATATCCAAAAGCACACC 377
QY 747 AGTAATGATGAAAAAGAGAGGAAAAATTATCAATTCATCTGTAGTTGGTCTTAC 806
Db 378 ACAAAATGTTAAGACAACGTTAGTGGTCTATCATCAATTTATCAAGTGTGTTGGAGCAGT 437
QY 807 TGGCAATGTTGCCAAGCTAATATAGCCAGCCAGGCTGGAGTGTATGGTTTACAAA 866
Db 438 AGGTAATCGGACAGCAAACTATGTTGCAACAAAAGCAGGTGTTATGGTTTAACTAA 497
QY 867 AACAGTTCGACGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGACACAGGGTT 926
Db 438 ATCTCGGGCGGTGAATGACATCTCTGTGTATCACTGTAAATGACGTGGACCTGGTTT 557
QY 927 CATTCATCTGATGACTGCCGAAGCTTCGGAAGAGCTTGGAAGAAATCTTGTCAAC 986
Db 558 TATTGTTCTGATATGACAGATGCTTAAAGTGTATGAGCTTAAAGAACAAATGTTGACTCA 617
QY 987 CATTCGGTTAGGAGATATGGCAACCAAGAGGAGTTCAGGGTTGGTGCAGTTCCTGSC 1046
Db 618 AATTCGGTTAGCACGTTTGGTCAAGACACAGATATTGCTAATACAGTAGCGTCTTAGC 677
QY 1047 CCTTAACCCCGACGCTAGCTATATGACTGCACAGGTGCTTACAAATTCAGCGAGGATGTT 1106
Db 678 ATCAGA---CAAGCAAAATATATTACAGTCAACATCCATGTTAAATGGTGGATGTA 734
QY 1107 AATGTAA 1113
Db 735 CAIGTAA 741

RESULT 12

AA55365
ID AA55365 standard; DNA; 741 BP.
AC AA55365;
XX
DT 13-FEB-2002 (first entry)
XX
DE Staphylococcus aureus DNA for cellular proliferation protein #1677.
XX
DE Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.

XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR P-PSDB; AAU37506.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Claim 27; Seq ID No 9002; 511pp; English.

XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 741 BP; 261 A; 104 C; 167 G; 209 T; 0 other;

Query Match 17.9%; Score 237.4; DB 23; Length 741;
Best Local Similarity 58.9%; Pred. No. 8.4e-40;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 387 TGTTCCTTACAGTCTAGAGGATGTTAGGCAACTGCTCTAGCCCTTGGAAA 446
Db 18 TGTTCCTTACAGTCTAGAGGATGTTAGGCAACTGCTCTAGCCCTTGGAAA 77
QY 447 AGCAGGATGCAAGTTCGTGTAACATGTCGCCGCTCTCGAAGAGGCTGAGAGGCTCTC 506
Db 78 AGAAGGATATATGATGAGCAGTAACTATGCGAGCGCAAGAGAGCTGAGAGCAGTAGT 137
QY 507 CAAGAGATGCAAGCTCTGTTGAGGCTATCACCTTCGAGGAGAGTGTTCACAAA 566
Db 138 CGAAGAAATCAAGCTAAAGGTGTTGACAGTTCGAGTTCAGCAAAATGTTCCGATGC 197
QY 567 AGCTGATGATGATCTATGATGAAGAGCAGCTCTAGATAAATGGGGAACAATGATGTGCT 626
Db 198 TGATGAAGTTAAGCAATGATTTAAAGAGTAGTCTAGCCAAATTTGGTCTCTTAGATGTTT 257
QY 627 GGTAAATATGCGAGGATGACAGACACATGTTGATGAGATGAGAAATCTCAGTG 686
Db 258 AGTAAATATGCGAGTATTACTCGCGATAATTTAATGCGTATGAAAGAACAGAGTG 317
QY 687 GCAAGACGTAATGATCTGAATCTTACTGGCGCTCTTCTTTGTACACAGGCTGCAACAA 746
Db 318 GGATGATGTTATGACACAACTTAAAGTGTATTTAACTGATATCCAAAAGCACACC 377
QY 747 AGTAATGATGAAAAAGAGAGGAAAAATTATCAATTCATCTGTAGTTGGTCTTAC 806
Db 378 ACAAAATGTTAAGACAACGTTAGTGGTCTATCATCAATTTATCAAGTGTGTTGGAGCAGT 437
QY 807 TGGCAATGTTGCCAAGCTAATATAGCCAGCCAGGCTGGAGTGTATGGTTTACAAA 866
Db 438 AGGTAATCGGACAGCAAACTATGTTGCAACAAAAGCAGGTGTTATGGTTTAACTAA 497
QY 867 AACAGTTCGACGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGACACAGGGTT 926
Db 438 ATCTCGGGCGGTGAATGACATCTCTGTGTATCACTGTAAATGACGTGGACCTGGTTT 557
QY 927 CATTCATCTGATGACTGCCGAAGCTTCGGAAGAGCTTGGAAGAAATCTTGTCAAC 986
Db 558 TATTGTTCTGATATGACAGATGCTTAAAGTGTATGAGCTTAAAGAACAAATGTTGACTCA 617
QY 987 CATTCGGTTAGGAGATATGGCAACCAAGAGGAGTTCAGGGTTGGTGCAGTTCCTGSC 1046
Db 618 AATTCGGTTAGCACGTTTGGTCAAGACACAGATATTGCTAATACAGTAGCGTCTTAGC 677
QY 1047 CCTTAACCCCGACGCTAGCTATATGACTGCACAGGTGCTTACAAATTCAGCGAGGATGTT 1106

```
Db 678 ATCAGB---CAAGCAAAATATTATACAGTCAACAATCCATGTAATGGTGGATGTA 734
QY 1107 AATGTAA 1113
Db 735 CATGTAA 741

RESULT 13
AAS51824
ID AAS51824 standard; DNA; 738 BP.
AC AAS51824;
XX
DT 13-FEB-2002 (first entry)
DE
DE Staphylococcus aureus DNA for cellular proliferation protein #241.
XX
XX Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
XX Staphylococcus aureus.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US09180.
XX
XX 21-MAR-2000; 2000US-191078P.
XX
XX 23-MAY-2000; 2000US-206848P.
XX
XX 26-MAY-2000; 2000US-207727P.
XX
XX 23-OCT-2000; 2000US-242578P.
XX
XX 27-NOV-2000; 2000US-253625P.
XX
XX 22-DEC-2000; 2000US-257931P.
XX
XX 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
XX
XX P-PSDB; AAU33965.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Claim 27; Seq ID No 4406; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 738 BP; 261 A; 106 C; 165 G; 206 T; 0 other;
XX
XX Query Match 17.9%; Score 236.8; DB 23; Length 738;
XX Best Local Similarity 59.5%; Pred. No. 1.1e-39;
XX
```

```
Matches 400; Conservative 0; Mismatches 272; Indels 0; Gaps 0;
QY 388 GTTGTGTTACAGGTGTCATCTAGAGGGATGTAAGGCAACTGCTCTAGCCCTTGAATAA 447
Db 19 GCTTTAGTAACACAGGTGTCATCAAGAGGAATTGGACGTAGTATTGCGTTACAATTAGCAGAA 78
QY 448 GCAGGATGCAGGTTCTGTTAACTATGCCCGTCTCGAAGAGGCTGGAAGGTCCTCC 507
Db 79 GAAGGATATATGTAGCAGTAACTATGCAGCACAAGAAAAAGCTGAAGCAGTATGTC 138
QY 508 AAAGAGATTGAAGCATCTGGTGGTCAAGCTATCACTTCGGAGAGAGATGTTTCAAAAGAA 567
Db 139 GAAGAAATCAAGCTAAAGGTGTTGACAGTTTTCGATTCAGCAAAATGTTGCCGATGCT 198
QY 568 GCTGATGTAGACTCTATGATGAAGACAGCTCTAGATAAATATGGGAAACAATAGATGTGTCG 627
Db 199 GATGAAGTTAAAGCAATGANTTAAGAAGTAGTTAGCCAAATTTGTTCTTTAGATGTTTAA 258
QY 628 GTAAATATGCGAGGATTACAGACACACATTTGTTGATGAGGATGAAGAAATCTCAGTGG 687
Db 259 GTAAATATGCGAGGTATTACTCGCATATTTATTAAATGCGGTATGAAGAACAAGAGTGG 318
QY 688 CAAGACGTAATGATCTGAATCTTACTGGCGTCTTCTTTGTACACAGGCTGCAACAAA 747
Db 319 GACGATGTTATTGACACAAACTTAAAGGTGTTATTAACTGTATCCAAAAGCAACACCA 378
QY 748 GTAATGTGAATAAGAGAAAGGAAAAAATTATCAATTCATTCGATCTGTAGTTGGTCTTACT 807
Db 379 CAAATGTTAAGACAACAGTAGTGTCTATCATCAATTTATCAAGTGTGTTGGAGCAGTA 438
QY 808 GGCATGTTGGCCAAAGCTAATTATAGCGCAGCAAGGCTGGAGTGAATTCGTTTCAAAAA 867
Db 439 GGTATTCAGGACAAGCAAACTATGTTGCCAACAAGCAGGTGTTATGTTGGTTAACTAAA 498
QY 868 ACAGTTGCGCAGGAGTATGCAAGCAGAAATATCAATGTGAATCTTATTCACACAGGTTTC 927
Db 499 TCTGGCGCGTGAAATAGCATCTCGTGTATCACTGTAATGCACTGCACCTGCTTTT 558
QY 928 ATTGCATCTGATATGATCTCCGCACTTGGAGAGAGCTTGGAGAAATCTTGTCAACC 987
Db 559 ATTGTTTCTGATATGACAGATGCTTTAAGTATGAGCTTTAAAGAACAAATGTTGACTCAA 618
QY 988 ATTTCGTTAGGAGATATGCGCAACCCAGAGGAGTTGCGAGGTTGGTTCAGTTCCTGGCC 1047
Db 619 ATTCCGTTAGCAGTTTGTGTCAGACACAGATATTCCTAATACAGTAGCGTCTTAGCA 678
QY 1048 CTTAACCCCGCA 1059
Db 679 TCAGACAAAAGCA 690

RESULT 14
ABT14915
ID ABT14915 standard; DNA; 929 BP.
XX
XX AC ABT14915;
XX
XX DT 06-MAR-2003 (first entry)
XX
XX Pathogen specific antigen related staphylococcal DNA SEQ ID No 117.
XX
XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
XX hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
XX auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
XX autoimmune disease; HIV; hepatitis; gene; ds.
XX
XX Staphylococcus sp.
XX
XX WO200259148-A2.
XX
XX PD 01-AUG-2002.
XX
XX 21-JAN-2002; 2002WO-EP00546.
```


Best Local Similarity 56.3%; Pred. No. 4.4e-38;
Matches 447; Conservative 0; Mismatches 336; Indels 3; Gaps 1;

QY	377	AAGCTCCAGTGTGTGTGTACAGGTGTCATCTAGAGGGATGTTGGTAAGGCAACTGCTCTAG	436
Db	180922	AAGGCAAGTAGCAGTAGTAACAGGTGGATCGCGGGAATCGTCTGTGACATGCCATCA	180981
QY	437	CCCTTGGAAAGCAGGATGCAAGTCTTGTTAACTATGCCCCGGTCTCTGAAAGAGGCTG	496
Db	180982	AATTAGCTAAAGAAAGCGCAATATTTCTTCAATTACAATGGTAGCCCGAGAGCTGCGG	181041
QY	497	AAGAGTCTCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATCACCTTCGGAGGAGATG	556
Db	181042	AAGAAACAGCAAAACTCGTTCGCGACATGGTGTAGAGTAGAAGCAATGAAGCAACG	181101
QY	557	TTTCAAAAGAAAGCTGATGTAGATCTATGATGAAGCAGCTCTAGATAAATGGGGAACAA	616
Db	181102	TAGCGATTGCTGAAGATGTGATGCTATTTTCAAAACAAGCAATCGAGCGCTTTGGTCGTA	181161
QY	617	TAGATGTGCTGGTAAATAATGCAAGGATTAACAGACACATTTGTTGATGAGGATGAAGA	676
Db	181162	TCGACATTTTAGTCAATAATGCGGGAATTACGGGTGATAATTTATTAAATGCGAATGAAG	181221
QY	677	AATCTCAGTCGCAAGAGTGAATTTGATCTGAATCTTACTGGCGTCTTCCTTTGTACACAGG	736
Db	181222	AAGCGAGTGGATGACGTTATTAAATCAATCACTTAAGCACTTTCCTTTGTACAAAG	181281
QY	737	CTGCAACAAAGTAATGATGAAGAAAGAGAAAGGAAATTAATCAACATTCGATCTGTAG	796
Db	181282	CAGTAAGTCGTACATGATGAACCAACGCGCTGGTAAATTTATCAACATGGCTTCGTGG	181341
QY	797	TTGGTCTTACTGGCAATGTTGGCCAGCTAATTATAGCGAGCAAGCTGGAGTGATTCG	856
Db	181342	TTGGCTTAATTTGGTAATGCGGGTCAAGCAAACTATGTTGCAAGTAAAGCAGGGGTAATTG	181401
QY	857	GTTCACAAAACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTG	916
Db	181402	GTTTACAAAACAACTGCTCGTGAATGTTGTCACGTTGTTAATGCTTCTGTTG	181461
QY	917	CACGAGGTTCAATGCTATGATGATGCTGCGAACTTGGAGAAAGAGCTTGAGAGAAAA	976
Db	181462	CTCCTGGTTTCATTACACAGAAATGACAGACAAATTAGATGATAAAACAAAGAGCAA	181521
QY	977	TCITGTCAACCATTCGGTAGGAGATATGCCAACAGAGAGATTGCGGGTTGGTCG	1036
Db	181522	TGCTAGCTCAAAATTCGGTTCGCTTACGGAAACACCGAAGATATTGCGAATGCGATT	181581
QY	1037	AGTTCTCTGGCCCTTAAACCCCGCAGTAGCTATATGACTGGACAGTGTCTACAATTGACG	1096
Db	181582	TTTTCTTAGC---AAGCGATGATCGAAGTATATTACTGGCCAAACACTATCCGTTGATG	181638
QY	1097	GAGGATGGTAATGTAAGATTGAGTTGATGCACTTCTACTTTTGGCTGAGCATTT	1156
Db	181639	GCGGAATGGTAATGTAAATTTGGTTAATGAATGCAATTTACTTGGCTCGCATTTTA	181698
QY	1157	AATGTT 1162	
Db	181699	AATATT 181704	

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Job time : 409 secs

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OM nucleic - nucleic search, using sw model

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Searched: 569978 seqs, 220691566 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	489.2	36.9	1185	3 US-08-793-035-1	Sequence 1, Appli
2	488.8	36.9	1155	3 US-08-793-035-2	Sequence 2, Appli
3	237.4	17.9	741	3 US-09-238-481-1	Sequence 1, Appli
4	237.4	17.9	741	4 US-09-572-810A-1	Sequence 1, Appli
5	217.2	16.4	19702	4 US-08-961-527-7	Sequence 7, Appli
6	215	16.2	750	4 US-09-134-001C-1988	Sequence 1988, Ap
7	211.8	16.0	732	4 US-09-239-052-1	Sequence 1, Appli
8	184.4	13.9	1196	4 US-08-858-207A-8	Sequence 8, Appli
9	179.8	13.6	768	4 US-09-107-532A-1296	Sequence 1296, Ap
10	153.2	11.6	1830121	4 US-09-557-884-1	Sequence 1, Appli
11	153.2	11.6	1830121	4 US-09-643-990A-1	Sequence 1, Appli
12	150.4	11.3	5395	4 US-09-221-017B-383	Sequence 383, App
13	139.4	10.5	10303	4 US-09-634-238-410	Sequence 410, App
14	139.4	10.5	1230025	4 US-09-198-452A-1	Sequence 1, Appli
15	132.8	10.0	867	4 US-09-252-991A-1887	Sequence 1887, Ap
16	132.8	10.0	1089	4 US-09-252-991A-2074	Sequence 2074, Ap
17	132	10.0	789	4 US-09-328-352-635	Sequence 635, App
18	126.2	9.5	474	4 US-09-724-623-23	Sequence 23, Appl
19	117	8.8	4403765	3 US-09-103-840A-2	Sequence 2, Appli
20	117	8.8	4411529	3 US-09-103-840A-1	Sequence 1, Appli
21	112.8	8.5	6977	4 US-08-178-257-8	Sequence 8, Appli
22	112.8	8.5	804	4 US-08-134-001C-2205	Sequence 2205, Ap
23	110.4	8.3	1723	1 US-08-241-766-1	Sequence 1, Appli
24	110.4	8.3	1723	1 US-08-241-766-2	Sequence 2, Appli
25	110.4	8.3	2232	1 US-08-241-766-12	Sequence 12, Appli
26	110.4	8.3	3120	1 US-08-491-146-1	Sequence 1, Appli
27	110.4	8.3	3120	1 US-08-241-766-11	Sequence 11, Appli

Sequence 1, Appli
Sequence 1, Appli
Sequence 1675, Ap
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 9, Appli
Sequence 191, App
Sequence 12, Appl
Sequence 3, Appli
Sequence 10, Appl
Patent No. 5229279
Patent No. 5512669
Sequence 10188, A
Sequence 10, Appl
Sequence 1151, Ap
Sequence 24, Appli
Sequence 2, Appli

28 110.4 8.3 3120 1 US-08-234-011-1
29 110.4 8.3 3120 2 US-08-701-062A-1
30 109 8.2 792 4 US-09-134-001C-1675
31 102.8 7.8 786 4 US-09-468-738A-28
32 102.8 7.8 786 4 US-09-940-019-28
33 102.8 7.8 786 4 US-09-940-037A-28
34 102.6 7.7 3252 4 US-09-672-749-9
35 100.6 7.6 15393 4 US-09-453-702B-191
36 98.2 7.4 2675 4 US-09-636-791A-12
37 94.8 7.1 1721 1 US-08-241-766-3
38 94.8 7.1 3051 1 US-08-241-766-10
39 94 7.1 2044 6 5229279-3
40 94 7.1 2094 6 5512669-3
41 92.6 7.0 1311 4 US-09-252-991A-10188
42 90.8 6.8 2535 4 US-09-672-749-10
43 89.2 6.7 828 4 US-09-107-532A-1151
44 87.6 6.6 741 1 US-08-241-943-24
45 87.6 6.6 990 1 US-08-254-357-2

ALIGNMENTS

RESULT 1
US-08-793-035-1
; Sequence 1, Application US/08793035
; Patent No. 6011201
; GENERAL INFORMATION:
; APPLICANT: Siabas, Antoni R.
; APPLICANT: White, Andrew
; APPLICANT: Chase, Dianne
; APPLICANT: Elborough, Keiran
; APPLICANT: Fenem, Phillip A.
; TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
; TITLE OF INVENTION: Brassica Napus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,035
; FILING DATE: 28-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9414622.2
; FILING DATE: 20-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB95/01678
; FILING DATE: 17-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: MOBT:132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713.787.1400
; TELEFAX: 713.787.1440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1185 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-793-035-1

QY 507 CAAAGAGATTGAAGCATCTCGTGGTGGAGGTATCACTTCGGAGGAGATGTTTCAAAGA 566
Db 138 CGAAGAAATCAAAGCTAAAGGTGTGACAGCTTTTGGCAATCAAGCAAAATGTCGGATGC 197
QY 567 AGCTGATGTAGATCTATGATGAAGCAGCTCTAGATAATGGGACCAATAGATGCT 626
Db 198 TGATGAAGTTAAAGCAATGAATGAAGAGTAGTAGCCAAATTTGGTTTATAGATGCTT 257
QY 627 GGTAAATATCGAGGATACAGCAGACACATTTGATGAGGATGAAGAAATCTCAGTG 686
Db 258 AGTAATAATCGAGGTATTAATCGGATATTTATTAATCGGATGAAGAACAGAGTG 317
QY 687 GCAAGAGCTAATGATCTGAATCTTACTGGCGTCTTCCCTTTGTACACAGGCTGCAACAA 746
Db 318 GGATGATGTTATTGACACAACTTAAAGGTGATTTAACTGTATCCAAAAAGCAACACC 377
QY 747 AGTAATGATGAAGAGAGAGGAAATATCAATTCATCTGCTAGTTGCTCTTAC 806
Db 378 ACAATGTTAAGACACAGTAGTGTCTATCATCAATTTATCAAGTGTGTTGGAGCAGT 437
QY 807 TGGCAATGTTGGCCCAAGCTAATTATAGCGCAGCCAGGCTGGAGTGAATGTTTCAAAA 866
Db 438 AGTATCCGGGACAGCAAACTATGTTGCAACAAAGCAGGTGTTATTGTTTAACTAA 497
QY 867 AACAGTTGCCAGGAGATGCAAGCAGAAATATCAATGTGATGCTATTGACACAGGTT 926
Db 498 ATCTGCGCGCGTGAATAGCATCTCGTGGTATCACTGTAAATGCACTTGCACCTGGTT 557
QY 927 CATTGCACTGATGATGACTGCGCAACTTTGGAGAGAGCTTGAGAGAAATCTTGTCAAC 986
Db 558 TATTGTTCTGATATGACAGATGCTTTAAGTGATGAGCTTAAGAACAAATGTTGATCA 617
QY 987 CATTCCGTTAGGAGATATGCCCAACAGAGAAAGTTGCGAGGTTGTCAGTTCTTCGGC 1046
Db 618 AATTCCGTTAGCAGTTTGGTCAAGACACAGATATTGCTAATACAGTAGGTTCTTAGC 677
QY 1047 CCTTAACCCGACCTAGCTATGATGCTGAGCAGGCTGCTTCAATGACGAGGAGGT 1106
Db 678 ATCAGA---CAAAGCAAAATATTTACAGGTCAAAACCAATCCATGTAATGTTGGAATGTA 734
QY 1107 AATGTAA 1113
Db 735 CATGTAA 741

RESULT 5

US-08-961-527-7/c
; Sequence 7, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-7

Query Match 16.4%; Score 217.2; DB 4; Length 19702;
Best Local Similarity 57.5%; Pred. No. 5.6e-41;
Matches 437; Conservative 0; Mismatches 308; Indels 15; Gaps 2;
QY 353 TTGTAAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACAGGTGATCTAGAG 412
Db 16209 TTGAAAGGAAAAAATGAACACTAGAACATAAAATAATCTTTATTCAGGTTCCAGTCGTG 16150
QY 413 GGATTGCTAAGGCAACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGGTTCTGGTAAACT 472
Db 16149 GAATTGCTTTCCTCCATCGCCCAAGTTTGTCTCAAGCAGGACCAATTTGCTTAAACA 16090
QY 473 ATGCCCGGTCCTGAAAGAGGCTGGAAGAGGTCTCCAAAGAGATTGAAGCATCTGGTGGT 532
Db 16089 GTCGTGGGG- - - - -AATCTCAGAAAGAAATTTGCTGCTGAGTTTCAAACTATGTTATCA 16036
QY 533 AGCTATCACTTCGAGGAGGATGTTTCAAAAGAGCTGATGATGATGATGATGATGATG 592
Db 16035 AGTGTGTTCCATTTTCAGGAGATGTTATCAGATTTTGCAGACGTTAAGCTGATGATGATC 15976
QY 593 CAGCTCTAGATAAATGGGAAACAATAGATGCTGCTGTTAAATAATACAGGAGATTACAGAG 652
Db 15975 AAGCTATTGCAAGAACTGGGTTTCAGTAGATGTTTGGTCAACAATGAGGAGATTACCAAG 15916
QY 653 ACACATTTGATGAGATGAAGAAATCTCAGTGGCAAGACGCTAAATGATCTGAATCTTA 712
Db 15915 ATACTCTTATGCTCAAGATGACAGAAAGCAGATTTTGAAGAAAGTCTCAAGGTCATCTGA 15856
QY 713 CTGGCGTCTTCCTTTGTACACAGGCTGCACAAAGTAATGATGAAAGAGAAAGGAA 772
Db 15855 CTGGTGCCTTTAATATGACACAATCAGTCTTGAAGACCGATGATGAAGCCAGAGAGGTG 15796
QY 773 AAATTATCAACATTTGATCTGTAGTTGGTCTTACTGGCAATGTTGGCCAAAGCTAATTA 832
Db 15795 CTATCATTAATATGCTAGTGTGTTGGTGTGATGGGAAATATTGTTCAAGCTAATATG 15736
QY 833 GCGCAGCAAGGCTGGAGTGAATGTTTCAAAAACAGTTGCCAGGAGTATGCAAGCA 892
Db 15735 CTGCTTCAAGGCTGGGTTGATTTGGCTTTTCAAGTCTGTGGCAGCGAGGTCTAGTC 15676
QY 893 GAAATATCAATGATGATGCTATTGACACAGGTTTCAATTGATCTGATGATGATGATGATG 952
Db 15675 GGAATATACGAGTCAATGATTTGCTCCAGAAATGATTTAGTCTGATGATGATGATGATG 15616
QY 953 TTGGAAGAGAGCTTTGAGAAGAAATCTTGTCAACCAATTCGTTAGGGAGATATGCCAAC 1012
Db 15615 TGTCAATAGATTAAGAGAGCTACACTAGCTCAGATTCGATGAAGAAATTTGGCAGG 15556
QY 1013 CAGAGGAGTTGCAAGGTTTGGTTCAGTCTCTGGCCCTTAACCCCGAGTATGATGATGA 1072
Db 15555 CAGAGCAGGTTGCAGATTTGCACAGTATTTTATG-----CAGGCAAGATTTATCTAA 15505
QY 1073 CTGGACAGGCTTACAAATTCAGGAGGATGTTAATGTA 1112
Db 15504 CTGGACAGGTTGTTGCCAATTTGATGTTGCTTAAATGTA 15465

RESULT 6

US-09-134-001C-1988
; Sequence 1988, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1988
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1988

Query Match 16.2%; Score 215; DB 4; Length 750;
Best Local Similarity 56.9%; Pred. No. 4.7e-41;
Matches 414; Conservative 0; Mismatches 310; Indels 3; Gaps 1;

QY 387 TGTGTTGTGTACAGGTGCACTAGAGGATTTGTAAGGCACTGCTCTAGCCCTTGGAAA 446
DB 27 TCGTTTGTGTACAGGTGCTCTCGTGTATTTGTAAGCAATTCGAATTCGCGA 86
QY 447 AGCAGATGCAAGGTTCTGTAACTATGCGCGTCTCGAAAGCGCTGAAGAGTCTC 506
DB 87 AGAGATATATGTAGTGTCAATTTATGCTGAAGTAAGATAAGCAGAGCACTTGT 146
QY 507 CAAAGAGATTAAGCATCTGCTGGTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAA 566
DB 147 TGAAGAAATTTAAAGCTAAAGGCTAGAAAGCTTTGCAATACAAAGCAAGTTCGAA 206
QY 567 AGCTGATGTAGCTCTATGATGAAGCAGCTCTAGTAATGAGGCAATAGATGCT 626
DB 207 CGATGAAGTTAAAGAAATGATTAAGAGTGGTAAGTCACTTTGGTTCTGTAGATG 266
QY 627 GGTAAATATGACGGGATTAACAGACACATTTGTTGATGAGGATGAAGAAATCTCAG 686
DB 267 GGTAAATATGAGGATTAACAGACACATTTGTTGATGAGGATGAAGAAATCTCAG 326
QY 687 GCAAGACGTAAATGATCTGATCTTACTGCGCTCTTCTTTGATGACAGGCTGCAAAA 746
DB 327 GGATGACGTGATGATACGAACTTAAAGGCGTGTAACTGTATTTCAAAAAGTAACGC 386
QY 747 AGTAATGATGAAGAAAGGAAAGAAATATCAATTTGATGATGATGATGATGATGAT 806
DB 387 ACAATTTGCGTCAACGTATGCTGCAATTTAATTTAATTTAATTTAATTTAATTTA 446
QY 807 TGGCAATTTGGCCAACTAATTTATAGCGAGCAAGCTGGAAGTATGTTTTCAAA 866
DB 447 GGGTAATCTGGCAACCAACTATGTTGCAACAAAGCAGGTGTCATTTGATTAACAA 506
QY 867 AACAGTTGCCAGGAGATGCAAGCAGAAATATCAATGTAATGTAATGTAATGTAATG 926
DB 507 AACTGACGACGAGAACTAGCATCACGAGGTATTTACAGTGAACGCTTAGCACCTG 566
QY 927 CATTGATCTGATGATGCTGCGCACTTGGAGAGGCTTGGAGAGGATTTGTAAGGAT 986
DB 567 CATCGTTTCAAGATCAAAATGCTTTAAGTATGATTTGAAGGATCAAAATGTTAGACA 626
QY 987 CATTCCGTTAGGAGATATGCCAACAGAGGAGTTCAGGGTTCGAGTTCCTGGC 1046
DB 627 AATTCCCTTAAACGTTTGGAGAGATACAGATATAGCTTAATCTGTCCTTAGC 686
QY 1047 CCTTAACCCGACGTAGCTATATGACTGGACAGGCTGCTTACAAATGACGAGGAGT 1106
DB 687 TTCTGA---TAAAGCTAAATATATTACAGGCCCAACCAATTCATGTTAACGGTGAAT 743

QY 1107 AATGTAA 1113
DB 744 TATGTAA 750

RESULT 7
US-09-239-052-1
; Sequence 1, Application US/09239052
; Patent No. 6346395
; GENERAL INFORMATION:
; APPLICANT: Holmes, David J.
; APPLICANT: Zhong, YiYi
; APPLICANT: Debouck, Christine
; APPLICANT: Jaworski, Deborah D.
; APPLICANT: Wang, Min
; APPLICANT: Warren, Richard L.
; APPLICANT: Kosmatka, Anna L.
; APPLICANT: McDevitt, Damien
; APPLICANT: Ingraham, Karen A.
; APPLICANT: Chalker, Alison F.
; APPLICANT: So, Chi Young
; APPLICANT: Wallis, Nicola G.
; APPLICANT: Pearson, Stewart C.
; TITLE OF INVENTION: Fabg
; FILE REFERENCE: GM10191
; CURRENT APPLICATION NUMBER: US/09/239,052
; CURRENT FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-239-052-1

Query Match 16.0%; Score 211.8; DB 4; Length 732;
Best Local Similarity 58.2%; Pred. No. 2.6e-40;
Matches 394; Conservative 0; Mismatches 277; Indels 6; Gaps 1;

QY 370 AGCTGGAAGCTCCAGTGTGTTGTTTACAGTGATCTAGAGGATTTGGTAAGCAACT 429
DB 4 AAACATAGACATAAAAAATATCTTTATACAGGTCGAGTCGTAAGTTCCTTGCATC 63
QY 430 GCTCTAGCCCTTGGAAAGCAGATGCAAGTTCGTTAAACTATGCCCGTCTCGAAA 489
DB 64 GCCACAGATTGCTCAGCAGAGGCAACATGCTTTAAACAGTCTGCGGC-----A 117
QY 490 GAGGCTGAAGAGGCTCTCCAAAGAGATTGAAGCATCTGGTGAGGCTATCACCTTCGGA 549
DB 118 ATCTCAGAAGAAATGCTCGCTGAGTTTCAAACATATGTTATCAAGGTGCTTCCCATTTCA 177
QY 550 GGAGATGTTTCAAAGAGCTGATGTAGTCTATGATGAAGCAGCTCTAGATTAATGG 609
DB 178 GGAGATGTATCAGATTTTTCAGACGCTAAGCGTATGATTTGATCAAGCTATTCAGAACTG 237
QY 610 GGAACAATAGATGCTGCTGTTAAATATGAGGATTTACAGGATTTACAGACACATTTGATGAG 669
DB 238 GGTTCAGTATGATGTTTGTTCACATGAGGATTTACCAAGATCTCTTATGCTCAAG 297
QY 670 ATGAAGAAATCTCAGTGGCAAGCGTAATTTGATCTGAAATCTTACTGGGCTTCTTCTTGT 729
DB 298 ATGACAGAAGCAGATTTTGAAGAAAGTCTCAAGGTCAATCTGACTGCTGCTTAAATATG 357
QY 730 ACACAGCTGCAACAAAGTAATGATGAAGAGGAAAGGAAATTTATCAATTTGCA 789
DB 358 ACACAATCAGTCTTGAACCCGATGATGAAGCCAGAGAGGCTCTATCATTAATATGTCT 417
QY 790 TCTGTAGTGTCTTACTGCTCAATGTTGCGCAAGCTAATTTATAGCGCAGCAAGGCTGA 849
DB 418 AGTGTGTTGTTGATTTGGGAAATATTTGTCAGAGCTAACTATGCTGCTTCTAAGGCTG 477
QY 850 GTGATTTGGTTTCAAAAAACAGTTGCCAGGAGTATGCCAGGAGATATCAAGCAGAAATATCAAT 909

478 TTGATTGGCTTTACCAAGTCTGTGGCAGCGAGGTGCTAGTGGGAATATACGAGTCAAT 537
QY 910 GCTATTGGACACCGGTTTCATTGTCATCTGATATGACTGCCGAACTTGGAGAGAGCTTTGAG 969
Db 538 GTGATTGCTCCAGGATGATTGAGTCTGATATGACAGCTATCTTATCAGATAGATTAG 597
QY 970 AGAAAAATCTGTCAACCATTCCTCGTTAGGAGATATGGCCAACAGGAGGAGTTGACGG 1029
Db 598 GAAGCTACACTAGCTCAGATTCGATCAAGAAATTTGGGCGAGCAGAGGTTGCAGAT 657
QY 1030 TTGGTCGAGTCTCTGGC 1046
Db 658 TTGACAGTATTTTAGC 674

RESULT 8

US-08-858-207A-8
; Sequence 8, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-858-207A-8

Query Match 13.9%; Score 184.4; DB 4; Length 1196;
Best Local Similarity 58.4%; Pred. No. 7.9e-34;
Matches 362; Conservative 0; Mismatches 251; Indels 7; Gaps 2;

QY 353 TTGTAAGAAGTGTACCAAGCTGGAAGTCTCAGTGTGTGTTTACAGGTCATCTAGAG 412
Db 572 TTGAAGGAAAAAATGAACTAGAACATAAAATATCTTTTATACAGGTTGAGTCGTG 631
QY 413 GGATTGGTAAGGCAACTGCTCTAGCCCTTGGAAAAGCAGGATGCAAGGTTCTGGTAAACT 472
Db, 632 GAATTGGTCTGGCCATCGCCACAGTTTGTCTCAGCAGGAGCCACATTGCTTTAACA 691

QY 473 ATGCCCGTCTCGAAAGAGGCTGAAGAGGTCTCAAAGAGATTGAAGCATCTGGTGGT 532
Db 692 GTCGTGGGCG-----AATCTCAGAAGAATTGCTCGCTGAGTTTCAAACCTATGTTATCA 745
QY 533 AGGCTATCACCTTCGGAGGAGATGTTTCAAAGAGAGCTGATGTAGAGTCTATGATGAAG 592
Db 746 AGGTGGTTCCTCCATTTTCAGAGAGATGATCAGATTTTGCAGACGCTAAGCGTATGATGATC 805
QY 593 CAGCTCTAGATAAATGGGGAACAATAGATGTCTGCTGTAATAATGACAGGGATTACACGAG 652
Db 806 AAGCTATTGCAGAACTGGGTTTCAGTAGATGTTTGGTCAACAATGCAGGGATTACCCAAG 865
QY 653 ACACATTTGTTGATGAGATGAAGAAATCTCAGTGCAGACGCTAATGATCTGAATCTTA 712
Db 866 ATACTCTTTATGCTCAAGATGCAGAAAGCAGATTTTAAAAAAGTGTCAAGGTCATCTGA 925
QY 713 CTGGGCTCTTCCTTTGTATACACAGGCTGCACAAAAAGTAAATGATGAAAAAGAGAAAGGAA 772
Db 926 CTGGTGCCCTTTAATATGACAAATCAGTCTTGAACCGATGATGAAGCCAGAGAGGTG 985
QY 773 AAATTATCAACATTCGATCTGTAGTTGGTCTTTACTGGCAATGTTGGCCAAAGTAAATATA 832
Db 986 CTATCATTAATATGCTAGTGTGTTGGTTTCATGGGGAATATTGTCAGGCTAACTATG 1045
QY 833 GGCAGCCAGCTGAGTGAATGTTTTCACAAAAACAGTTCGCCAGGAGTATGCAAGCA 892
Db 1046 CTGCTCTTAAGGCTGGCTTGGCTTTACCAAGTCTGTGGCAGCGAGGTCGCTAGTC 1105
QY 893 GAAATATCAATGTGAATGCTATTGCACACAGG-GTTCATTGCACTCTGATGATGCTGCCGAA 951
Db 1106 GGAATATACGATGATGATGCTCCAGGAAATGATGCTGATATGACAGCTATC 1165
QY 952 CTGGAGAGAGCTTGAGAA 971
Db 1166 TTATCAGATAAGATTAAAGGA 1185

RESULT 9

US-09-107-532A-1296
; Sequence 1296, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007


```
TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 1296:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...768
; SEQUENCE DESCRIPTION: SEQ ID NO: 1296:
US-09-107-532A-1296

Query Match 13.6%; Score 179.8; DB 4; Length 768;
Best Local Similarity 54.8%; Pred. No. 7.8e-33; Indels 15; Gaps 2;
Matches 411; Conservative 0; Mismatches 327;

QY 362 ATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACAGTGCATCTAGAGGGATTGGTA 421
Db 26 ACCTTATGGATGTAAGAGGAAAAATGTTATTCACAGGTAGTACAAAGAGGAATCGCA 85
QY 422 AGGCAATGCTCTAGCCCTTGGAAAAGCAGGAGTGCAGTCTGTGTTAACTATGCCGGT 481
Db 86 AAGCGATGGCTTAGCTTTTGCAAAAGCTGGAGCAAAATATCATTTGAATGGTCGGGAG 145
QY 482 CCTCGAAGAGGCTGAAGAGTCTCCAAAGAGATTGAAGCATCTGGTGGTGAAGCTATCA 541
Db 146 -----AGATCCAAAAGAAAAGATGAGAAATCGAAGCATTCGGGTGTAATGCGTAG 199
QY 542 CCTCGAGGAGATGTTTCAAAAGAGCTCATGTAGAGTCTATGATGAAGAGAGCTCTAG 601
Db 200 GAGTTCCGGTGACATCTCTGATTATGAGAAGCGGACAAATGATCAAGAGCAGAAG 259
QY 602 ATAAATGGGGAACAATAGATGTGCTGTTAAATATGAGGAGTACAGGAGACATGT 661
Db 260 AAAAGCTTGGATGCATCCATGTGTAGTAAACAATGCGGAATCACAATGACAACTG 319
QY 662 TGATGAGATGAAGAAATCTCAGTGGCAAGACGTAATGATCTGAATCTTACTGGCGTCT 721
Db 320 TGATGCAATGGATGCAAGATTTCAAAAATATGCTGGAATCATTTGATTGGAACCT 379
QY 722 TCCTTTGTACACAGGCTGCAAAAAGTAATGATGAAAAGAGAAAGGAAAATTTATCA 781
Db 380 TCAATATGCGCAGCAGCTATTGAAAAAATGATGAGCAGGAGAGGGGCCATCATTA 439
QY 782 ACATTGATCTGTAGTTGGTCTTACTGGCAATGTTGGCAAGCTAAATATAGCCAGCCA 841
Db 440 ATCTCTAGTGTATCTGGGTGTGTTGAAATATTTGCTCAGCAAAATTTATGCACTAGTA 499
QY 842 AGGCTGAGTGATTTGTTTCAAAAACAGTTGCGCAGGAGTATGCAAGCAGAAATATCA 901
Db 500 AAGCTGGCGTAGTAGGATTAACAATCTGTGGCAACGAGAGCTGCAACTAGAGCAATTA 559
QY 902 ATGTGAATGCTATTGCGCAGGGTTCATPTGTCATCTGATGATGATGATGATGATGATG 961
Db 560 CATGTAATGCCATTGCGCAGGATTCATCACAACTGATATGATGATGATGATGATGATG 619
QY 962 AGCTTGAAGAAAATCTTGTCAACCATTCCTGTTAGGAGATATGGCCAAACCAAGGAG 1021
Db 620 AAGTCAAGGAACAAGCGGAAAAGCAATTCGGATGTCAGCGGTTTCGGCAAGTAGAATA 679
QY 1022 TTGCAAGGTTGTCGAGTCTCTGCTGCTTACCCCGCAGCTAGTATATGATGATGATGATG 1081
Db 680 TTGCACAAACGCGAGTTTCTTAGCAAAAATCC-----ATATATACCCGCAAG 730
QY 1082 TGCTTAAATTTGACGAGGGATGGTAATGTAAG 1114
Db 731 TCATCAATGTCGATGGCGGATTTGTCATGACG 763
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RESULT 10

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US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof
;
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/557,884
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,102
; FILING DATE: JUN-5-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB186P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1830121 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
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Query Match 11.6%; Score 153.2; DB 4; Length 1830121;
Best Local Similarity 52.0%; Pred. No. 3.1e-25;
Matches 397; Conservative 0; Mismatches 354; Indels 12; Gaps 2;

QY 370 AAGCTGGAAGCTCCAGTTGTTGTTTACAGGTCATCTAGAGGATTTGTAAGGCAACT 429
Db 171555 AAAATGCAGGTAAAAATGCTTTAGTGACAGGATCTACCCGTGTTATCGGTGCGGATT 171496
QY 430 GCTCTAGCCCTCGAAAAGCAGGATCAAGGTTCTGTAACTATGCCGGTCTCGAAA 489
Db 171495 GCAGAAGAACTTAGTTCAAAAGG-----TGCATTTGTTATTTGGTACAGCAACTCTGAA 171442
QY 490 GAGGCTGAAGAGGTCTCCAAAGAGATTTGAAGCATCTGGTGGTGAGGCTATCACCTTCGGA 549
Db 171441 AAGGTCAGAGCGGATCTCGGCTTAT-----TTAGGGGATAAAGTAAAGGTTTAGTT 171388
QY 550 GGAGATGTTTCAAAAGAGCTGATGTAGTCTATGATGTAAGAGCAGCTCTAGATAAATGG 609
Db 171387 TTAACCGTAACGGATAAAGAACTCTATCGAAACCTTACTTGAACAAATTAATAAATGATTTT 171328
QY 610 GGAACATAGATGCTGCTGTTAAATATGAGGATTTACAGAGACATTTGTTGATCAGG 669
Db 171327 GGCATATTGATATTCTCGTGAATAACGCGAGTATTACTCGCATTAATTTATTGATCGGT 171268
QY 670 ATGAAGAAATCTCAGTGGCAAGACGTAATGATCTGAATCTTACTGCGCTTCTCCTTTGT 729
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Db 171267 ATGAAGAAGAGGAATGGTTGATATATATGCAAACTAACTTAACCTGGTGTATCATCTT 171208
Qy 730 ACACAGGCTCAACAAAAGTAATGATGAAAAGAGAAAGGCAAAAATTAACAATGCA 789
Db 171207 TCTAAGCCATGTACCTCAATGATGAAAACGTTTGGTGTATCATCATATTTGGT 171148
Qy 790 TCTGTAGTTGGTCTTACTGCAATGTTGGCAAGCTAAATATAGCGAGCGCAAGGCTGGA 849
Db 171147 TCAAGTGGTTGGTTCACAGGTAATCCAGAGCAAACTAACTATTTGGTGGCAAAAGCGGT 171088
Qy 850 GTGATTTGGTTCAAAAAGAGTTCAGGAGAGTATCAAGCAGAGATATCAATGTGAAT 909
Db 171087 GTGGTTGGTTTCTTAAATCTTTAGCGAAAGAGTAGCTGCACGTGTATTTACTGTAAAT 171028
Qy 910 GCTATTGACAGGAGTTCATTCGATCTCATATGATGCTGCCAACTTTGGAGAGAGCTTTGAG 969
Db 171027 GTGGTTGGTCTCTGTTTATTTGCAACAGATATGACAGAGTGTCTTACGGATGAACMAAA 170968
Qy 970 AAGAAATCTTGTCAACATTCCTGTAGGAGATATGGCCACAGAGAGAGTTGCGAGG 1029
Db 170967 GCGGGATCTTATCTAATGTTCCAGCTGGACGTTTAGCGAAGCNAAGACATAGCTAAA 170908
Qy 1030 TTGTCGAGTTCCTGGCCCTTAACCCGCGAGCTAGCTATATGACTGGACAGGTGCTTACA 1089
Db 170907 GCGGGATCTTATCTAATGTTCCAGCTGGACGTTTAGCGAAGCNAAGACATAGCTAAA 170908
Qy 1090 ATTGACGAGGAGTGTAAATGAAGATTGAGTTAGCTTGTATG 1132
Db 170847 AATGGTGCCTTACTTAAAGCTAAATTTGACATTTGATG 170805

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RESULT 11

US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289

GENERAL INFORMATION:

APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter

TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186PIC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Query Match 11.6%; Score 153.2; DB 4; Length 1830121;
Best Local Similarity 52.0%; Pred. No. 3.1e-25;
Matches 397; Conservative 0; Mismatches 354; Indels 12; Gaps 2;

```

Qy 370 AGCTGGAAGCTCCAGTGTGTTGTTTACAGTGCACTAGAGGGAATTTGGTAAGGCAACT 429
Db 171555 AAAATCAAGGTAAATTTCTTTAGTGACAGGATCTACCCGTTGATCGGTGCGATT 171496
Qy 430 GCTCTAGCCCTTGGAAAAGCAGGATGCAAGGTTCTGGTAAACTATATCCCGGTCTCTCGAA 489
Db 171495 GCAGAAAGAACTTAGTTCAAAAGG-----TGCATTTGTAATTGGTACAGCACTCTGAA 171442
Qy 490 GAGGCTGAAGAGGTCTCCAAAGAGATTGAAGCATCTGGTGGTGAAGCTATCACCTTCGGA 549
Db 171441 AAGGTTGACAGAGCGGATCTCGGCTTAT-----TTAGGGGATAAAGGTAAAGGTTAGTT 171388
Qy 550 GAGATGTTTCAAAAGAAAGCTGATGTAGTCTATGATGAAGCAGCTCTAGTAATAATGG 609
Db 171387 TTAACGTTAACGGATAAAGAACTATCGAAACCTTACTTGAACAAAATTAATAATGATTTT 171328
Qy 610 GGAACAATAGATGCTGCTGTAAATAATGAGGAGATTACAGGAGATTACAGACACATTTGATGAGG 669
Db 171327 GCGGATATTGATTAATCTCTGTAATACGCAAGTATTACTCGCGATAATTTATTGATGCGT 171268
Qy 670 ATCAAGAATCTCAGTGGCAAGACGTTAATGATGCTGAATCTTACTGCGCTCTTCCTTTGT 729
Db 171267 ATGAAGATGAGGAATGGTTTGATATTAATGCAAACTAACTTAACCTCGGTGTATCATCTT 171208
Qy 730 ACACAGGCTCAACAAAAGTAATGATGAAAAGAGAAAGGAAAAATTAACAATTTGCA 789
Db 171207 TCTAAGCCATGTAGCTTCAATGATGAAAAGAGGTTTGGTGTATCATCAATTTGGT 171148
Qy 790 TCTGTAGTTGGTCTTACTGGCAATGTGGCAAGCTAATATATAGCGAGCAAGGCTGGA 849
Db 171147 TCAAGTGGTTGGTTCACAGGTAATCCAGCAAACTAATCTATTTGGCGCAAAAGCGGT 171088
Qy 850 GTGATTTGGTTTCAAAAACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAAT 909
Db 171087 GTGGTTGGTTTCTTAAATCTTTAGCGAAAGAGTAGCTGCACGTGTATTTACTGTAAAT 171028
Qy 910 GCTATTGACAGGAGTTCATTCGATCTGATATGATGCTGCCAACTTTGGAGAGAGCTTTGAG 969
Db 171027 GTGGTTGGTCTCTGTTTATTTGCAACAGATATGACAGAGTGTCTTACGGATGAACMAAA 170968
Qy 970 AAGAAATCTTGTCAACCAATTCGGTTAGGGAGATATGCCAACACAGAGAGAGTTGCGAGG 1029
Db 170967 GCGGGATCTTATCTAATGTTCCAGCTGGACGTTTAGCGAAGCNAAGACATAGCTAAA 170908
Qy 1030 TTGTCGAGTTCCTGGCCCTTAACCCGCGAGCTAGCTATATGACTGGACAGGTGCTTACA 1089
Db 170907 GCGGTTGGTTTCTTAAATCTTCTGATGATGAGGTATATATCAGCGGAACAAACGTTACAGTG 170848
Qy 1090 ATTGACGAGGAGTGTAAATGAAGATTGAGTTAGCTTGTATG 1132
Db 170847 AATGGTGCCTTACTTAAAGCTAAATTTGACATTTGATG 170805

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RESULT 12

US-09-221-017B-383/c
Sequence 383, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

```

;
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA: Pp1182
; APPLICATION NUMBER: Pp1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Pp1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA: Pp2911
; APPLICATION NUMBER: Pp2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 383:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5395 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORYPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...5395
; US-09-221-017B-383

Query Match 11.3%; Score 150.4; DB 4; Length 5395;
Best Local Similarity 51.2%; Pred. No. 1.3e-25;
Matches 377; Conservative 0; Mismatches 356; Indels 3; Gaps 1;

QY 385 GTTGTGTTGTTGTTACAGGTGATCTAGAGGGATTGGTAAGGCACTGCTTAGCCCTTGA 444
DB 1558 GTAGCTCTATTACGGGACGGGCGGTATCGCGGTGCTATAGTATGCA 1499

QY 445 AAAGCAGATGCAAGTTCTGGTAACTATGCCCGGTCTCGAAAGAGGCTGAAGAGTC 504
DB 1498 ACGGAAGGTGCGGATGTGGCTATTACTGATCTGAATATCGATGAGGCGGTACAGGCTTTC 1439

QY 505 TCCAAAGAGATTGAAGCATCTGGTGGTGAGGCTATACCTTCGGAGGAGATGTTTCAAAA 564
DB 1438 GTAGAAGAACTCAAGGGCTCGGAGTAGCTGACGGGCAATACGCTTCCATGACGGGAT 1379

QY 565 GAAGCTGATGATGATCTTATGATGAAAGCAGCTCTAGATAAATGGGAAACAATAGATGTG 624
DB 1378 TTCCATGACGACATACAGATGCTGGTGAACAGATCAAGGCTGACTTCGGTCCGATCATATT 1319

;
; US-09-634-238-410/c
; Sequence 410, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410
; LENGTH: 10303
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; US-09-634-238-410

Query Match 10.5%; Score 139.4; DB 4; Length 10303;
Best Local Similarity 52.8%; Pred. No. 6.1e-23;
Matches 350; Conservative 0; Mismatches 306; Indels 7; Gaps 2;

QY 395 TTACAGGTGATCTAGAGGATTGGTAAGCAACTGCTCTAGCCCTTGGAAAACGAGGAT 454
DB 6999 TCACCGTGTCTCACGAGGTATCGGTGAAGCGATTGCCAGAAATTTGCTCAAGCAGGG 6940

;
; 625 CTGGTAAATAATGACAGGATTACAGACACATTTGTTGATGAGGATGAAGAAATCTCAG 684
; 1318 TTGGTGAACAATGCCGGTATTACTCGCATGGCCTTATGATGCGTATGCCAGCAACA 1259
; 685 TGGCAAGACGTAATTGATCTGAATCTTACTTGTGCGCTTCTTTGTACAGGCTGCAACA 744
; 1258 TGGGATGCCGTGATCAACGTTAACTCTGAAGTCAGCGTTCAACATGATCCATGCCGTGACT 1199
; 745 AAAGTAATGATGAAAAAGAGAAAGGAAAAATTATCAACATTTGATCTGTTGTTGTT 804
; 1198 CCCATCATGATGGGACACGCGCAGTATCATCAATATGCTTCTGTGTAGGTGTA 1139
; 805 ACTGCGCAATGTTGGCCAAAGCTAATTATAGCGCAGCAAGGCTGGAGTGAATTTGTTTCA 864
; 1138 TCAGGCAATGACGACCAATCACTACTCAGCTTCTTAAGCCGGTATGATCGTTTGGCC 1079
; 865 AAAACAGTTGCCAGGGAGTATGCAAGCAGAAATATCAATGTGAATGCTTATGCAACAGGG 924
; 1078 AAGAGTGTGCCAAAGAGCTGGGCTCAGCTGCGTGGTGGTCCCAATCGGATTGCACCGGCT 1019
; 925 TTCAITGATCTGATATGACTGCCGAACTTGAGAGAGAGCTTGAGAGAAATCTTGTCA 984
; 1018 TTTATCATCACCGATATGACTGCCGTCTTACGGAAGAGTGAAGAACAATGGCGGCA 959
; 985 ACCATTTCGTTAGGAGATATGCGCAACACAGAGGAGTTGCAGGGTTGGTCAGTTCTCTG 1044
; 958 CAGATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
; 1045 GGCCTTTAACCCGCGAGCTAGCTATATGACTGACAGAGGCTTCAATATGACAGGAGGATG 1104
; 898 GGCAGTGACCTC--TCTTCGTACGTGACGCGGACAGGTAGTCCACGTTTGTGGCGGTATG 842
; 1105 GTAAATGATGATTTGA 1120
; 841 AATATGTAATATATAGGA 826
;
; RESULT 13
; US-09-634-238-410/c
; Sequence 410, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410
; LENGTH: 10303
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; US-09-634-238-410

Query Match 10.5%; Score 139.4; DB 4; Length 10303;
Best Local Similarity 52.8%; Pred. No. 6.1e-23;
Matches 350; Conservative 0; Mismatches 306; Indels 7; Gaps 2;

QY 395 TTACAGGTGATCTAGAGGATTGGTAAGCAACTGCTCTAGCCCTTGGAAAACGAGGAT 454
DB 6999 TCACCGTGTCTCACGAGGTATCGGTGAAGCGATTGCCAGAAATTTGCTCAAGCAGGG 6940
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/ NAME/KEY: misc feature
/ LOCATION: (420001)..(435000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc feature
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/ LOCATION: (510001)..(525000)
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/ LOCATION: (720001)..(735000)
/ OTHER INFORMATION: n=a or c or g or t
/ NAME/KEY: misc feature
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/ OTHER INFORMATION: n=a or c or g or t

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; LOCATION: (810001)..(825000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (825001)..(840000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (840001)..(855000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (855001)..(870000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (885001)..(900000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature

Query Match 10.5%; Score 139.4; DB 4; Length 1230025;
Best Local Similarity 53.3%; Pred. No. 4.4e-22;
Matches 318; Conservative 0; Mismatches 276; Indels 3; Gaps 1;

Qy 519 AGCATCTGGTGGTGAGGCTATCACCTTCGGAGAGATGTTTCAAAAGAACTGATGATGAGA 578
Db 344918 AGGCTGGGTGGCGAAGTTTCTTTTGTCTGTGTGATGTGAGTCATAATGGTGAGTGAA 344859

Qy 579 GTCTATGATGAAGACGAGCTCTAGATAAATGGGAACATAGATGTGCTGTAATATATGC 638
Db 344858 AGATTGCGTGCAGAAATTTTATAGTAAGCAACAAATAATATTTTGTGTAATATATGC 344799

Qy 639 AGGGATTACACGAGACACATTTGTTGATGAGATGAAGAAATCTCAGTGCGCAAGACGTAAT 698
Db 344798 AGGCATTACCGGATTAATTTGTTGATGCGTATGCTGAGAGACGACTGGCAATCGGTGAT 344739.

Qy 699 TGATCTGAATCTTACTGGCGTCTTCCCTTTGTACACAGGCTGCAACAAAGTAATGATGAA 758
Db 344738 TAGCACCACCTTGACTTCTCTTATATACATGTTCTCAGTGATTGCCATATGATTA 344679

Qy 759 AAGAGAAAGGAAATATTAACATTCATCTGTAGTTGGTCTTACTGCAATGTTGG 818
Db 344678 GGCAGCGTTTCAGGATCTATTAATAATGTTGCTTCTATTGTTGCTAAGATCGGTAGTGGGG 344619

Qy 819 CCAAGCTAATTATAGCGCAGCAAGGCTGAGTGATTGGTTTCAAAAAACAGTTGCCAG 878
Db 344618 CCAGACCACTATGCTGCTCTCTAAAGCTGGATTTGCTTTTCAAAAACTTTTAGCTAA 344559

Qy 879 GGAGTATGCAAGCAGAAATATCAATGTAATGTAATTTGCACCAGGTTTCAATGCAATCBA 938
Db 344558 GGAAGTAGCTGCAAGAAATATTCGTGTCAACTGCTTGTCTCCAGGCTTTTATTGAACAGA 344499

Qy 939 TATGACTGCCGAACCTTGGAGAAGCTTGAAGAAATCTTGTCAACCAATTCGTTAGG 998
Db 344498 CATGACAAGCGTGTGTAATGACAAATTTAAAGTGAGTGGCTTAAGTCGATCCCTTTAGG 344439

Qy 999 GAGATATGGCCACACGAGGAAGTTGCGAGGTTGGTCGAGTCTCTGCGCCCTTAACCCCGC 1058
Db 344438 TAGGGCTGGCACTCCAGAGATGTTGCTCTGTGGCGCTTTGTTTTAGCC---TCGCGATT 344382

Qy 1059 AGCTAGCTATATGACTGGACAGGTTGCTTACAATTAAGCAGGAGGATGTAATGTAAGA 1115
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RESULT 15

US-09-252-991A-1887/c
; Sequence 1887, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1887
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1887

Query Match 10.0%; Score 132.8; DB 4; Length 867;
Best Local Similarity 50.0%; Pred. No. 7.6e-22;
Matches 360; Conservative 0; Mismatches 357; Indels 3; Gaps 1;

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QY	402	TGCATCTAGAGGATTTGGTAGGCACTGCTTAGCCCTTGGAAAAACAGATGCAAGGT	461
DB	748	CGCCAGCCGTGGCATCGGCCAGGCGATTTGGCTGGAATCTGGGGCGCTGGGTGCCGTGT	689
QY	462	TCGTGTAATATATCCCGGTCTCGAAAGAGGCTTGAAGAGGTCTCCAAAGAGATTGAAGC	521
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QY	522	ATCTGGTGGTAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGAGTGATGAGATC	581
DB	631	CAATGGCGTCCAGGGTGGGGCTGGTCTCTGGAGGTTTCCAGCGACGAATCCGTAGCCGC	572
QY	582	TATCATGAAGCAGCTCTAGATTAATGGGGAACATAGATGTGCTGCTTAATATGCAGG	641
DB	571	GACCTGGAGCACATCCAGCAGCATCTCGGCCAACCGCTGATCGTGGTCAATAACGCCG	512
QY	642	GATTACACGACACATTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAATTGA	701
DB	511	CATCACCGCGATTAATCTGCTGGTGGCATGAAAGACGACGAGTGGTTCGATGTGTCAA	452
QY	702	TCTGAATCTTACTGGCGTCTTCTTTGTACACAGGCTGCAAAAGTAATGATGAAAAA	761
DB	451	CACCAACCTGAACAGTCTCTACCGTCTGTCTGAAAGCCGTTCTGGCGCGTATGACCAAGC	392
QY	762	GAGAAAGGAAAAATATACATGCTATCTGTAGTTGGTCTTACTGGCAATGTGCCA	821
DB	391	CCGCTGGGGCGGCATCATCAACATCGGTTCGTTGGTGGGCCCATGGGCAATCCGGGCA	332
QY	822	AGCTAATTATAGCGCAGCAAGGCTGGAGTGATTTGTTTCAAAAAACAGTTGCCAGGA	881
DB	331	AACCACTATGCCGGCGAAGCGCGCTGGAGGGCTTCAACCGTGGCTGGCCGGGA	272
QY	882	GTATGCAAGCAGAAATATCAATGTGAATGCTATTGCAACAGGGTTCAATTGATCTGAT	941
DB	271	AGTGGTTTCGGTGCCTTACCGTGAATGCGGTGGCGCGGGCTTTCATCGACACCGCAT	212
QY	942	GACTCCGAACTTGAGAGAGCTTGAGAGAAATCTTGTCAACCATTCGTTAGGAG	1001
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Db 151 CCTGGGGCAGCGGAAGAGATCGCCAAGGTGTGGCTTCCTCGCTTCGGAACGGCGCAGC 92

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 14:49:09 ; Search time 441 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Capext 1.0

Searched: 2141354 seqs, 1595478879 residues

Total number of hits satisfying chosen parameters: 4282708

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1326	100.0	1326	12	US-10-024-806-1
2	607.4	45.8	1286	12	Sequence 1, Appli
3	431.2	37.0	1398	12	Sequence 3, Appli
4	449.4	33.9	1248	12	Sequence 5, Appli
5	239.8	18.1	6251	8	Sequence 7, Appli
6	238	17.9	741	9	Sequence 25, Appli
7	237.4	17.9	741	9	Sequence 8025, Ap
8	236.8	17.9	741	9	Sequence 9002, Ap
9	236.8	17.9	738	9	Sequence 4406, Ap
10	232.8	16.0	744	10	Sequence 6558, Ap
11	211.8	16.0	732	9	Sequence 9262, Ap
12	210.2	15.9	732	9	Sequence 9483, Ap
13	179	13.5	7916	10	Sequence 1, Appli
14	175.2	13.2	741	10	Sequence 8, Appli
15	173	13.0	6021	10	Sequence 458, App
16	171	12.9	537	10	Sequence 6537, Ap

17 166.6 12.6 738 9 US-09-815-242-6824
18 158.8 12.0 468 10 US-09-974-300-2287
19 156.8 11.8 735 9 US-09-815-242-6029
20 153.2 11.6 1830121 14 US-10-329-960-1
21 148.4 11.2 744 9 US-09-815-242-7417
22 147.4 11.1 729 9 US-09-815-242-6877
23 146.8 11.1 744 9 US-09-815-242-7245
24 142.8 10.8 804 10 US-09-895-913A-361
25 132.4 10.0 640681 10 US-09-790-988-1
26 130.6 9.8 744 9 US-09-815-242-7795
27 126.2 9.5 474 12 US-10-288-930-23
28 125.2 9.4 786 12 US-10-004-115A-27
29 125.2 9.4 786 12 US-10-327-108-11
30 119.4 9.0 1000 10 US-09-971-536-32
31 115.2 8.7 813 10 US-09-974-300-2254
32 112.2 8.5 1980 12 US-10-166-225A-177
33 109.6 8.3 958 10 US-09-880-107-1741
34 106.8 8.1 29729 10 US-09-070-927A-238
35 106.4 8.0 789 9 US-09-815-242-6500
36 104.4 7.9 714 9 US-09-823-901-3
37 104.4 7.9 714 14 US-10-175-696-15
38 104.4 7.9 1043 9 US-09-823-901-1
39 104.4 7.9 1043 14 US-10-175-696-13
40 102.8 7.8 786 10 US-09-940-037A-28
41 101.2 7.6 1089 14 US-10-119-926-96
42 101 7.6 717 14 US-10-156-761-6439
43 101 7.6 9025608 14 US-10-156-761-1
44 100.6 7.6 729 12 US-10-238-075-836
45 100.6 7.6 15393 14 US-10-114-170-191

ALIGNMENTS

RESULT 1

US-10-024-806-1
; Sequence 1, Application US/10024806
; Publication No. US20030167532A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; TITLE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/258,417
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)...(1110)
US-10-024-806-1

Query Match 100.0%; Score 1326; DB 12; Length 1326;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GCGCGAGCTTCCAAAGCCCCCGTCCCCCAATAGACTCTCCCATCCCGTCTGTGTC 60
QY 61 GTCAAGGCTCAATATCTCGGCTGCACTCTCAAGACACTGTGCTGCTGCTCCGC 120
Db 61 GTCAAGGCTCAATATCTCGGCTGCACTCTCAAGACACTGTGCTGCTGCTCCGC 120
QY 121 CTCTCTTGGCTCTCTTGGTCCCGTCCGACGCCCCCTCATGCCACCGCGCCGCCA 180

Db 121 CTCTCTTGGGCTCTTGGGCTCCCGAGCGCCCTCATGCGCCACCGCGCGCCACCGCA 180
Qy 181 GCAGCAGCAGCAGCTCTCTCCCGGCTGCGCGTGGAGCAGCCGCGGCGCGCGCTCC 240
Db 181 GCAGCAGCAGCAGCTCTCTCCCGGCTGCGCGTGGAGCAGCCGCGGCGCGCTCC 240
Qy 241 CGCGGGGGTTCGTACAGTTGGTGGAGGCGCGCGGCTTCTCTCCAGCTCGGGTCC 300
Db 241 CGCGGGGGTTCGTACAGTTGGTGGAGGCGCGCGGCTTCTCTCCAGCTCGGGTCC 300
Qy 301 GSCCGTGGGTTCTCTGCTGTGCAACCCATGTTGCTGTGAAACAAGCAGTTGAA 360
Db 301 GSCCGTGGGTTCTCTGCTGTGCAACCCATGTTGCTGTGAAACAAGCAGTTGAA 360
Qy 361 GATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACAGTGTCATCTAGAGGATTTGGT 420
Db 361 GATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACAGTGTCATCTAGAGGATTTGGT 420
Qy 421 AAGGCACTCTCTAGCCCTTGAAAGCAGGATGCAAGTTCTGTTAACTATGCCCG 480
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Qy 481 TCCTCGAAAGAGGCTGAAGAGTCTCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATC 540
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Qy 541 ACCTTCGAGGAGATGTTTCAAAAGAGCTGATGAGTCTATGATGAAGCAGCTCTA 600
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Qy 661 TTGATGAGGATGAAGAAATCTCAGTGGCAAGCCTAATTCATCTGAATCTTACTGGCGTC 720
Db 661 TTGATGAGGATGAAGAAATCTCAGTGGCAAGCCTAATTCATCTGAATCTTACTGGCGTC 720
Qy 721 TTCCTTTGTACACAGGCTGCAACAAAGTAAATGATGAAGAAAGGAAAGGAAATATC 780
Db 721 TTCCTTTGTACACAGGCTGCAACAAAGTAAATGATGAAGAAAGGAAAGGAAATATC 780
Qy 781 AAGTTGATCTGATGTTGTTCTTACTGGCAAGCTAATTCATCTGAATCTTACTGGCGTC 840
Db 781 AAGTTGATCTGATGTTGTTCTTACTGGCAAGCTAATTCATCTGAATCTTACTGGCGTC 840
Qy 841 AAGCTGGAGTGAATGTTTTCACAAACAGTTCGCGAGGATGCAAGCAGAAATATC 900
Db 841 AAGCTGGAGTGAATGTTTTCACAAACAGTTCGCGAGGATGCAAGCAGAAATATC 900
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Db 1321 AAAAAA 1326

RESULT 2
US-10-024-806-3
; Sequence 3, Application US/10024806
; Publication No. US2003016752A1
; GENERAL INFORMATION:
; APPLICANT: Zheng, Peizhong
; APPLICANT: Li, Chun Ping
; APPLICANT: Nichols, Scott E.
; TITLE OF INVENTION: Oar Polynucleotides, Polypeptides and
; TITLE OF INVENTION: Their Use in PHA Production in Plants
; FILE REFERENCE: 35718/241887
; CURRENT APPLICATION NUMBER: US/10/024,806
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)...(1050)
US-10-024-806-3

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Best Local Similarity 75.4%; Pred. No. 2.3e-140;
Matches 755; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

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Db 58 CTCCT 117
Qy 178 GCAGCAGCAGCAGCT 237
Db 118 GCGCTGCGCAGCAGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 177
Qy 238 TCCGCGCGGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
Db 178 GCGCGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 237
Qy 298 TCCGCGCGGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
Db 238 CGCGCGCT 297
Qy 358 AAGATCTTACCAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 417
Db 298 AAGATGATCAAGTTGGAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
Qy 418 GGTAAAGCACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGGTTCTGGTAAACTATGCC 477
Db 358 GGAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
Qy 478 CGGTCTCTCGAAGAGGCTGAGAGGCTCTCCAAAGAGATTGAAGCATCTGGTGGTGGCT 537
Db 418 CGATCTTCAAGGAGGCTGAGAGTCTCCAGAGATTGAAGCATCTGGAGGCCAGGCC 477
Qy 538 ATCACTCTCGAGAGAGATGTTTCAAGAGAGCTGATGATGATGATGATGATGATGATGAT 597
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; NAME/KEY: CDS
; LOCATION: (16)..(912)
HS-10-024-806-7

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	Query Match	33.9%;	Score 449.4;	DB 12;	Length 1248;
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Qy	404	CATCTAGAGGGAATTGGTAAGCAACTGCTTAGCCCTTGGAAAAAGCAGGAATGCAAGGTTTC	463		
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Qy	464	TGGTAAACTATGCCCGGTCTCGAAAGAGGCTGAGAGGCTCTCCAAAGAGNATGCAACAT	523		
Db	266	TGGTCAACTATGCCCAGGTCATCCCATGCAAGCTGAGGAGGTTTCAACTTGTGATGAGGCGT	325		
Qy	524	CTGGTGTGAGGCTATCAACCTTCGGAGGAGATGTTTCAAAAAGAAAGCTGATAGAGTCTA	583		
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Qy	584	TGATGAAGAGAGCTTAGATAAATGGGGAAACATAGATGTGCTGTGTTAAATTAATGACGGGA	643		
Db	386	TGATTAGAAGCTGCAGTTGATGCTTGGGGAACTGTGTTGATGTATTTGTTAAACAAATGCAGAA	445		
Qy	644	TTACACGAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGCTTAATGATC	703		
Db	446	TTACTCGAGATGGTTTGTTAATGAGAAATGAAGAAATCAATGGCAGGAGTATTATGATC	505		
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Qy	884	ATGCAAGCAGAAATATCAATGTGAATGCTATTATGCACCGGGTTCATTCGATCTGATATGA	943		
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Db	866	ATTACATCACTGGGCAGGTGTTTCCATTGATGAGGTTTGGCAATGTGAG	916		

STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIA TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 6251 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-25

RESULT 5
US-08-781-986A-25
; Sequence 25, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
;

QY 987 CATTCGGTTAGGAGATATGGCCACACAGAGAGAGTTGTCAGGGTGGTTCGAGTCTCTGC 1046
Db 4916 AATTCGGTTAGCAGCGTTTGGTCAAGACACAGATATTTGCTAATACAGTAGCGTTCTTAGC 4975
QY 1047 CCTTAACCCGAGCTAGCTATATGACTGCACAGGTCCTTACAAATGACGGAGGATGCT 1106
Db 4976 ATCAGAAAGCAAAATATATACAGGTCAACAAATCCATGTAATGGTGGATGTACAT 5035
QY 1107 AATGTAAGATTTGAGTTAGCTTGATGCATCTTCTATTTTCTGAGACATTAATGTTGAA 1165
Db 5036 GTAATATATTTGAGCTAAAGCTCATTCAGCGCTGGTGGTCTGCTATCCATGAGAA 5094

RESULT 6

US-09-815-242-8025

; Sequence 8025, Application US/09815242

; Patent No. US2002061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 8025

; LENGTH: 741

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(741)

; US-09-815-242-8025

Query Match 17.9%; Score 238; DB 9; Length 741;

Best Local Similarity 59.0%; Pred. No. 8.9e-49;

Matches 428; Conservative 0; Mismatches 295; Indels 3; Gaps 1;

QY 388 GTTCTGTTACAGTGATCTAGAGGATTTGGTAAGCACTGCTTAGCCCTGGAAAA 447
Db 19 GCTTTAGTAACAGGTGCTCAAGAGGATTTGGTATGCTTACATTAAGCAGAA 78
QY 448 GCAGATGCAGGTTCTGGTAACTATGTCGCGTCTCGAAGAGGCTGAAGGCTCTCC 507
Db 79 GAAGGATATATGATGACGATTAATCTGACGGCAGCAAGAAAGCTGAAGCAGTAGTC 138
QY 508 AAAGAGATTAAGCATCTTGGTGGTGGAGCTATCACCTTCGGAGGAGATGTTTCAAAAGAA 567
Db 139 GAAGGAATCAAGCTAAAGGTGTTGACAGTTCGATTCAGCAAAATGTTGCCGATGCT 198

QY 568 GCTGATGTAGAGTCTATGATGAAGACAGCTCTAGATAAATGGGGAACAATAGATGTGCTG 627
Db 199 GATGAAGTTAAAGCAATGATTAAGAGTAGTTAGCCAAATTTGGTCTTTAGATGTTTAA 258
QY 628 GTAAATAATGACAGGATTAACAGACACACATTTGTTGATGAGGATGAAGAAATCTCAGTGG 687
Db 259 GTAAATAATGACAGGATTAACAGGATTAATTTAAATGCGGTATGAAAGAACACAGAGTGG 318
QY 688 CAAAGAGTAATTTGATCTGAACTTACTGCGCTCTTCTTCTTGTACACAGCTCCACAAA 747
Db 319 GACGATGTTATTGACACAAACTTAAAGGTGTTTAACTGTATCCAAAAGCAACACCA 378
QY 748 GTAAATGATGAAGAGAGGAGGAAAAATTCAACATTCATCTGTAGTTCGTCTTACT 807
Db 379 CAATGTTAAGCAACAGTAGTGTGCTATCATCAATTTATCAAGTGTGTTGGAGCAGTA 438
QY 808 GCAATGTTGGCCAGCTAATTTATATGCGCAGCAAGGCTGGAGTGATTTGTTTCAAAA 867
Db 439 GGTAAATCCAGGACAAAGCAACTATTTGCAACAAAAGCAGGTGTTTATTTGTTTAACTAAA 498
QY 868 ACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTCAATGCTATTGCAACCGGTTTC 927
Db 499 TCTGCGGCGCGTGAATTAGCATCTCGTGTATCACTGTAAATGCAAGTTCGACCTGTTTT 558
QY 928 ATTGCATCTGATATGACTGCCGAACCTTGAGAGAGAGCTTGAGAAGAAAATCTTGTCAACC 987
Db 559 ATTGTTTCGATATGACAGATGCTTTAAGTGATGAGCTTAAAGACAAATTTGACTCAA 618
QY 988 ATTCCGTTAGGAGATATGCCCAACCCAGAGAGTTGCGAGGTTGGTCCAGTTCTTGGCC 1047
Db 619 ATTCCGTTAGCAGGTTTGGTCAAGACACAGATATTTGCTAATACAGTAGCGTCTTTAGCA 678
QY 1048 CTTAACCCTGAGCTAGCTATATGATGACAGGTCCTTACATTTACCGAGGAGTGA 1107
Db 679 TCAGA---CAAGCAAAATATATTACAGGTCAAAACAATCCATGTAATGTTGGAATGTAC 735
QY 1108 ATGTAA 1113
Db 736 ATGTAA 741

RESULT 7

US-09-815-242-8705

; Sequence 8705, Application US/09815242

; Patent No. US2002061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

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; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8705
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(741)
US-09-815-242-8705

Query Match      17.9%; Score 237.4; DB 9; Length 741;
Best Local Similarity 58.9%; Pred. No. 1.3e-48;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 387 TGTGTGTTGTACAGGTGCTCTAGAGGATTTGGTAAGGCAACTGCTCTAGCCCTTGGAAA 446
Db 18 TGCTTTAGTAACAGGTGCTATCAAGAGAAATGGACGTAGTATTGGTTACAATTAGCAGA 77
QY 447 AGCAGATGCAAGGTTCTGTGTAATGTCCTGAAAGAGGCTGAAAGGTC 506
Db 78 AGAAGGATATAATGTAGCAGTAACTATGTCAGGCAGCAAAAGAGAAAGCTGAAGCAGTAGT 137
QY 507 CAAAGAGATTGAGCATCTGGTGTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGA 566
Db 138 CGAAGAAATCAAGAGCTAAAGGTTGTGACAGTTTGGATTTCAAGCAAAATGTCGGATGC 197
QY 567 AGCTGATGTAGAGTCTATGATGAAAGCAGCTCTAGATAAATGGGAAACATAGATGTGCT 626
Db 198 TGATGAGTTAAGCAATGATTTAAGAGTAGTTAGCCAAATTTGGTTCTTTAGATGTTT 257
QY 627 GGTAAATAATGCAAGGATTACAGACACATTTGTTGATGAGATGAAGAAATCTCAGTG 686
Db 258 AGTAAATAATGCAAGGTATTACTCGCATTAATTTATTAATGCGTATGAAAGAACAGAGTG 317
QY 687 GCAAGAGTTAATGATCTGAATCTTACTGGCGTCTTCCCTTTGTACACAGGCTGCAACAAA 746
Db 318 GGATGATGTTATTGACACAACTTAAAGGTGTATTTAATGCGTATGAAAGAACAGAGTG 377
QY 747 AGTAATGATGAAAAGAGAAAGGAAAAATTTACAACTTGCATCTGTAGTGTGCTTAC 806
Db 378 ACAATGTTAAGACAAGTAGTGTGCTATCATCAATTTATCAAGTGTGTTGGAGCAGT 437
QY 807 TGGCAATGTTGGCCAAAGCTAATTTATAGCCAGCAAGGCTGAGTGTGTTTCAAAA 866
Db 438 AGGTAAATCCGGGCAAGCAAACTATGTTGCAACAAAAGCAGGTTTATGTTGTTAACTAA 497
QY 867 AACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAAATGCTATTGCAACAGGGTT 926
Db 498 ATCTGCGCGCGTGAATTAGCATCTCGTGTATCACTGTAAATGCACTGCACTGCTGTT 557
QY 927 CATTCATCTGATAGTATGCTCCGAACTTGGAGAGAGCTTGAAGAAATCTTGTCAAC 986
Db 558 TATTGTTCTGATATGACAGATGCTTTAAGATGATGAGCTTAAAGAACAAATGTTGACTCA 617
QY 987 CATTCCTGTAGGAGATATGCCAACAGAGAAAGTTGCAAGGTTGTCAGGTTCCNGGC 1046
Db 618 AATTCCGTTAGCAGTTTGGTCAAGACACAGATATTGCTAAATACAGTAGGTTCTTAGC 677
QY 1047 CCTTAAACCCAGCTATATGATGAGTGGACAGGTCGTTACAAATTCACGAGGAGGATGGT 1106
Db 678 ATCAGA---CAAGCAAAATATATTACAGGTCNAACATCCATGTAATGCGGAATGA 734
QY 1107 AATGTAA 1113
Db 735 CATGTAA 741

RESULT 8
US-09-815-242-9002
; Sequence 9002, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Truwick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9002
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(741)
US-09-815-242-9002
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Query Match      17.9%; Score 237.4; DB 9; Length 741;
Best Local Similarity 58.9%; Pred. No. 1.3e-48;
Matches 428; Conservative 0; Mismatches 296; Indels 3; Gaps 1;

QY 387 TGTGTGTTGTACAGGTGCTCTAGAGGATTTGGTAAGGCAACTGCTCTAGCCCTTGGAAA 446
Db 18 TGCTTTAGTAACAGGTGCTATCAAGAGAAATGGACGTAGTATTGGTTACAATTAGCAGA 77
QY 447 AGCAGATGCAAGGTTCTGTGTAATGTCCTGAAAGAGGCTGAAAGGTC 506
Db 78 AGAAGGATATAATGTAGCAGTAACTATGTCAGGCAGCAAAAGAGAAAGCTGAAGCAGTAGT 137
QY 507 CAAAGAGATTGAGCATCTGGTGTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGA 566
Db 138 CGAAGAAATCAAGAGCTAAAGGTTGTGACAGTTTGGATTTCAAGCAAAATGTCGGATGC 197
QY 567 AGCTGATGTAGAGTCTATGATGAAAGCAGCTCTAGATAAATGGGAAACATAGATGTGCT 626
Db 198 TGATGAGTTAAGCAATGATTTAAGAGTAGTTAGCCAAATTTGGTTCTTTAGATGTTT 257
QY 627 GGTAAATAATGCAAGGATTACAGACACATTTGTTGATGAGATGAAGAAATCTCAGTG 686
Db 258 AGTAAATAATGCAAGGTATTACTCGCATTAATTTATTAATGCGTATGAAAGAACAGAGTG 317
QY 687 GCAAGAGTTAATGATCTGAATCTTACTGGCGTCTTCCCTTTGTACACAGGCTGCAACAAA 746
Db 318 GGATGATGTTATTGACACAACTTAAAGGTGTATTTAATGCGTATGAAAGAACAGAGTG 377
QY 747 AGTAATGATGAAAAGAGAAAGGAAAAATTTACAACTTGCATCTGTAGTGTGCTTAC 806
Db 378 ACAATGTTAAGACAAGTAGTGTGCTATCATCAATTTATCAAGTGTGTTGGAGCAGT 437
QY 807 TGGCAATGTTGGCCAAAGCTAATTTATAGCCAGCAAGGCTGAGTGTGTTTCAAAA 866
Db 438 AGGTAAATCCGGGCAAGCAAACTATGTTGCAACAAAAGCAGGTTTATGTTGTTAACTAA 497
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QY 867 AACAGTTGCCAGGAGTATGCRAGCAGAAATATCAATGTGAATGCTATTGACACAGGTT 926
Db 498 ATCTGGGGCGCGTAATTAGTACTCTCGTGTATCACTGTAAATGCAAGTTGCACTGGTT 557
QY 927 CATTCATCTGATGACTCCGAACTTGGAGAGAGCTTGAGAGAAATCTTGTCAAC 986
Db 558 TATTGTTCTGATATGACAGATGCTTTAAGTGTAGCTTTAAGAACAAATGTTGACTCA 617
QY 987 CATTCGGTTAGGAGATATGCCAACACAGAGAGTGTGAGGTTGGTTCAGTTCCTGGC 1046
Db 618 AATTCGGTTAGCAGCTTTTGGTCAAGACACAGATATTGCTTAATACAGTAGCTTCTTAGC 677
QY 1047 CCTTAACCCGCGAGCTAGCTATATGCTGACAGAGTGTCTACAAATGACCGAGGAGTGT 1106
Db 678 ATCAGA---CAAGCAAAATATATTACAGGTCAAAACAAATCCATGTAAATGGTGAATGTA 734
QY 1107 AATGTAA 1113
Db 735 CATGTAA 741

RESULT 9

US-09-815-242-4406
; Sequence 4406, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITEA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4406
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4406

Query Match 17.9%; Score 236.8; DB 9; Length 738;
Best Local Similarity 59.5%; Pred. No. 1.8e-48;
Matches 400; Conservative 0; Mismatches 272; Indels 0; Gaps 0;
QY 388 GTTGTGTTACAGTGTGCTAGAGGGATTGTAAGGCAACTGCTTAGCCCTTGGAAA 447
Db 19 GCTTTAGTAACAGGTGCTAAGAGAAATGGACGTAGTATTGGCTTACAATTAGCAGAA 78
QY 448 CGAGATCAAGGTTCTGGTAAACTATGCCCGGCTCCTGAAAGAGGCTGAAGAGGTCTCC 507
Db 79 GAAGGATATATGTAGCACTTAACCTATCGAGGCAGCAAGAAAGCTGAAGCAGTAGTC 138

QY 508 AAAGAGATTGAAGCATCTGTTGGTGGAGCTATCACTTCGGAGGAGATCTTTCAAAGAA 567
Db 139 GAAGAAATCAAAGCTAAAGGTTGTCAGATTTCGGAATTCAGCAAAATTTGCCGATGT 198
QY 568 GCTGATGTAGAGCTATGATGAAGCAGCTCTAGATAAATGGGGAAACAATAGATGTGCTG 627
Db 199 GATGAAGTTAAAGCAATGATTAAGAGTAGTTAGCCAAATTTGGTCTTTTAGATGTTTA 258
QY 628 GTAATAATATGCGAGGATTAACAGAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTG 687
Db 259 GTAATAATATGCGAGGATTAATCTCGGATAATTTATTAATGCGTATGAAGAAACAAGAGTG 318
QY 688 CAAGCGTAATTTGATCTGATCTTACTGGCGCTCTCTCTTTGTACACAGGCTCAACAAA 747
Db 319 GACGATGTTATTGACACAAACTTAAAGGTGTATTTAACTGTATCCAAAAGCNAACCA 378
QY 748 GTAATGATGAAAAGAGAAAGGAAAATATCAACATTTGATCTCTAGTGTGCTTACT 807
Db 379 CAAATGTTAAGACACAGTAGTGTGCTATCATCAATTTATCAAGTCTTGTGGAGCAGTA 438
QY 808 GGCATGTTGGCCAGCTAATTAATGCGCAGCCAGGCTGGAGTGATTTGTTTCAAAA 867
Db 439 GGTAAATCCAGGACAGCAAACTATGTTGCAACAAAAGCAGGTGTTATTGTTTAACTAAA 498
QY 868 ACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCACAGGTTTC 927
Db 499 TCTGGCGCGGTGAATTAGCATCTCGTGTATCACTGTAATGCGATTTGCACTGTTT 558
QY 928 ATTGCATCTGATATGACTGCCGAACCTTGGAGAGAGCTTGAGAGAAAATCTTGTCAACC 987
Db 559 ATTGTTTCTGATATGACAGATGCTTTAAGTGATGACCTTAAAGAACAAATGTTGACTCAA 618
QY 988 ATTCCGTTAGGAGATATGCCAACACAGAGAAAGTTGCGAGGTTGTCGAGTTCTCTGGCC 1047
Db 619 ATTCCGTTAGCAGCTTTTGTGTCAGACACAGATATTGCTTAATACAGTAGGTTCTTAGCA 678
QY 1048 CTTAAACCCGCA 1059
Db 679 TCAGACAAAGCA 690

RESULT 10

US-09-974-300-6558
; Sequence 6558, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6558
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6558

Query Match 16.0%; Score 212.8; DB 10; Length 744;
Best Local Similarity 56.9%; Pred. No. 1.6e-42;
Matches 410; Conservative 0; Mismatches 307; Indels 3; Gaps 1;
QY 391 GTTGTACAGGTGATCTAGAGGATTTGTAAGCAACTGCTTAGCCCTTGGAAAAGCA 450
Db 22 GTTGTACAGCGCTTCAGCTGGAATTTGGCAAGCGATCGCCCTTGAACCTTGTGCTGCAAA 81


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/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9483
/ LENGTH: 732
/ TYPE: DNA
/ ORGANISM: Streptococcus pneumoniae
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(732)
US-09-815-242-9483

Query Match 15.9%; Score 210.2; DB 9; Length 732;
Best Local Similarity 58.1%; Pred. No. 7.1e-42;
Matches 393; Conservative 0; Mismatches 278; Indels 6; Gaps 1;

QY 370 AGCTGGAAGCTCAGTTGTTGTTTACAGGTGCTATAGAGGATGTTAGGCAACT 429
Db |||||
4 AAACATGAACATATAAATATCTTTATACAGGTTCGAGTCTGGAATGCTTTGCCATC 63
QY 430 GCTCTAGCCCTCGAAAGCAGGATGCAAGTTCTGGTAACTATGCCCGTCTCGAAA 489
Db |||||
64 GCCACAAAGTTTGCTCAAGCAGAGGCCACATTTGCTTTAAACAGTCTGGGGC-----A 117
QY 490 GAGGCTGAAGAGGCTCTCAAGAGATTAAGAGCTATCTGGTGGTGAAGGCTATCACCTTCGGA 549
Db |||||
118 ATCTCAGAAAGATTTGCTCGCTGAGTTTCAAACTATGTTATCAAGTGTTCCTCAATTCA 177
QY 550 GGAGATGTTTCAAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 609
Db |||||
178 GGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 237
QY 610 GGAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 669
Db |||||
238 GGTTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 297
QY 670 ATGAAGAAATCTCAGTGGCAGAGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 729
Db |||||
298 ATGACAGAGCAGATTTTGAAGAAAGTCTCAAGTCAATCTGACTGCTGCTGCTGCTGCTGCTGCT 357
QY 730 ACACAGCTGCAACAAAGTAAATGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789
Db |||||
358 ACACAAATCAGTCTTTGAAACCGATGATGAAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
QY 790 TCTGATGTTGCTTACTGCAATGTTGGCCAAAGCTAATTAATTAATTAATTAATTAATTAATTA 849
Db |||||

/ GENERAL INFORMATION:
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl L.
/ APPLICANT: Zyskind, Judith W.
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John D.
/ APPLICANT: Carr, Grant J.
/ APPLICANT: Yamamoto, Robert T.
/ APPLICANT: Xu, H. Howard
/ TITLE OF INVENTION: Identification of Essential Genes in
/ FILE OF INVENTION: Prokaryotes
/ FILE REFERENCE: ELITRA.011A
/ CURRENT APPLICATION NUMBER: US/09/815,242
/ CURRENT FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ NUMBER OF SEQ ID NOS: 14110
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9483
/ LENGTH: 732
/ TYPE: DNA
/ ORGANISM: Streptococcus pneumoniae
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(732)
US-09-815-242-9483

Query Match 13.5%; Score 179; DB 10; Length 7916;
Best Local Similarity 53.4%; Pred. No. 1.5e-33;
Matches 402; Conservative 0; Mismatches 345; Indels 6; Gaps 1;

QY 367 ACCAAGCTGGAAGCTCCAGTCTGTTGTTGTTACAGGTGCTATAGAGGATTTGTAAGGCA 426
Db |||||
4761 ACAACATTACAAGTTAAAGTAGCAATCGTAAACAGGCGGATCTAAAGGTATCGGGCAGCA 4820
QY 427 ACTGCTCTAGCCCTTGGAAAAGCAGGATGCAAGTTCTGGTAACTATGCCCGTCTCTCG 486
Db |||||
4821 ATTACAGGTGAGCTTCTTCTAATGGAGTAAAGTAGCAATCAACATTAACAGCAGTAA 4880
QY 487 AAAGAGCTGGAAGAGCTCTCCAAAGAGATTGAAGCATCTGGTGGTGAAGCTATCACCTTC 546
Db |||||
4881 GAATCTGCGAGAGCAATTTGAAGAAATTAAGACAACGCGCGAGAGCTATTCGGTT 4940
QY 547 GGAGAGATGTTTCAAGAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 606
Db |||||
4941 CAAAGTCAAGTCTTATGTATGATCAAGCAAAACACCTAATCGAAGAAACAAAAGCTGCG 5000
QY 607 TGGGGAACATAGATGCTGTTAAATATGAGGATGATGAGGATGATGAGGATGATGAGGATG 666
Db |||||
5001 TTTGGTCAATTAGACATCTTAGTAAACAAATGCTGGAATACGCGCAGCTTCATTCAAG 5060
QY 667 AGCATCAAGAAATCTCAGTGGCAAGCTAATTAATTAATTAATTAATTAATTAATTAATTA 726
Db |||||
5061 AAGTATGATGAGAGAGATTTGGAAGAAATTAATTAATTAATTAATTAATTAATTAATTAAC 5120
QY 727 TGTACACAGCTGCACAAAAGTAATGATGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
Db |||||
5121 ACAACATCAGCTGGCTAACGCCACCTTTTAGAATCTGAAGGTGCTGCTGTTTATCAATATT 5180
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QY 787 GCATCTAGTGTCTTACTGGCAATGTTGGCCAGCTAATTAATACGCGAGCAAGGCT 846
Db 5181 TCATCAATTAATGTCGAAGCGGGCGGATTTGGTCAAAACAATCTACTCAGCTGCTAAAGCA 5240
QY 847 GGAGTGTGTTGTTTCAAAAACAGTTGCCAGGAGATGCAAGCAGAAATATCAATGTG 906
Db 5241 GGTAGCTAGGATTCATTAATCATATTAGCTCTTGAATAGTACAGAGCGGTAAACGGTT 5300
QY 907 AATGCTAATGACAGGCTTCAATGCTATGATGATGCTGCGCAACTTGGAGAGAGCTT 966
Db 5301 AATGCAATTTGCCAGGATTAATGCAAAACGAAATGCTGATGGCAATTCCTGAAGATGT 5360
QY 967 GAGAGAGAAATCTTGTCAACCAATTCGTTAGGAGATATGGCCACACAGAGAGATGCA 1026
Db 5361 CGTGCAGAAATGTTGCGGAAATTCACACTGCTGCTTAGTCTACGCTGAAGAAATGCA 5420
QY 1027 GGGTGTGTCGAGTTCCTGGCCCTTAACCCCGCAGCTAGCTATATGACTGGACAGGCTT 1086
Db 5421 CGTGGAGTTGTTTACTTAGCAAAAGACGGCGC-----GTACATTACAGACACAGTTA 5474
QY 1087 ACAATGACGAGGATGTTAATGAAGTTG 1119
Db 5475 AACATTAACGCGGCTTATACATGTAATAAATG 5507
RESULT 14
US-09-479-040-8
; Sequence 8, Application US/09479040
; Publication No. US20020182690A1
; GENERAL INFORMATION:
; APPLICANT: McCool, Gabriel J.
; APPLICANT: Cannon, Maura C.
; APPLICANT: Cannon, Francis C.
; APPLICANT: Valentin, Henry E.
; APPLICANT: Gruys, Kenneth J.
; TITLE OF INVENTION: POLYHYDROXALKANOATE BIOSYNTHESIS ASSOCIATED PROTEINS
; FILE REFERENCE: WO8212
; CURRENT APPLICATION NUMBER: US/09/479,040
; CURRENT FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Bacillus megaterium
US-09-479-040-8
Query Match 13.2%; Score 175.2; DB 10; Length 741;
Best Local Similarity 53.3%; Pred. No. 3.5e-33;
Matches 369; Conservative 0; Mismatches 323; Indels 0; Gaps 0;
QY 367 ACCAAGCTGGAAGCTCCAGTTGTTGTTACAGGTGTCATCTAGAGGATTTGTAAGGCA 426
Db 4 ACAACATTACAAGGTAAAGTAGCAATCGTAACAGCGCATCTAAAGTATCGGGGAGCA 63
QY 427 ACTGCTTAGCCCTTGGAAAGCAGGATGCAAGTTCTGTGAATCTATGCCGCTCTCTCG 486
Db 64 ATTACAGTGTGCTTCTTAATGGAGTAAAGTAGCAGTAAATCTATAACAGCAGTAAA 123
QY 487 AAAGAGGCTGAAGAGTCTCCAAAGAGATTCAGCACTCTGTGTGAGGCTATCACCTTC 546
Db 124 GAATCTGCAAGCAATTTGTAAGAAATTAAGACACCGCGGAGAGCTATTGCGGTT 183
QY 547 GGAGGAGATGTTTCAAAAGAGCTGATGTAGTCTATGATGAAGCAGCTCTAGATAAA 606
Db 184 CAAGCTGACGTGCTTATGTAGTACAGCAAAACACCTAATCGAAGAACAAAGCTGCG 243
QY 607 TGGGGAACAATAGATGCTGTTAAATATGCGAGGATTAACGAGACACATTTGATG 666
Db 244 TTTGGTCAATTAGACATTTCTAGTAAACAATGCTGGAATTTAGCGCGACCGTTTCAAG 303

QY 667 AGGATGAAGAAATCTCAGTGGCAGAGCTAATTAATGATCTGAATCTTACTGGCTCTTCCT 726
Db 304 AAGTTAGGTGAAGAAATTTGAAAAAAGTAATTTGATGTAAACTTACATAGCGTATTACAAC 363
QY 727 TGTACACAGGCTGCAACAAAAAGTAATGATCAAAAAAGAGAAAGAAAAATTTATCAACATT 786
Db 364 ACACATCAGCTCGCTTAACGCACCTTTTAGAATCTGAGAGTGTGCTGTGTTATCAATATT 423
QY 787 GCATCTGTAGTTGGTCTTACTGTGCAATGTTGGCCAAAGCTAATTTATAGCGCAGCAAGGCT 846
Db 424 TCATCAATTAATTTGTCAGCGGCGGATTTGGTCAAAACAATCTACTCAGCTGCTAAAGCA 483
QY 847 GAGTGTGTTTCAAAAAACAGTTGCCAGGAGTATGCCAGCAGAAATATCAATGTG 906
Db 484 GGTATGCTAGGATTCATAATCATTAGCTCTTTGAACTAGTAAAGCAGCGCTAACCGTT 543
QY 907 AATGCTATTGACACAGGTTTCATTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 966
Db 544 AATGCAATTTGCCAGGATTTATTGAACGGAATGATGATGATGATGATGATGATGATGATGAT 603
QY 967 GAGAGAAATCTTGTCAACCAATTCGTTAGGAGATATGGCCAAACAGCAGAGGAGTTGCA 1026
Db 604 CGTGCAGAAATGTTGCGGAAATTCCAACTCGCTGCTTAGTCTACGCTGAAGAAATGCA 663
QY 1027 GGGTGTGTCGAGTTCTGCGCCCTTAACCCCGC 1058
Db 664 CGTGGAGTTGTTTACTTAGCAAAAGACGGCGC 695
RESULT 15
US-09-070-927A-458
; Sequence 458, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunsch
; Patrick J. Dillon
; Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 458:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6021 base pairs
; TYPE: nucleic acid


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; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 458:
US-09-070-927A-458

Query Match      13.0%; Score 173; DB 10; Length 6021;
Best Local Similarity 54.6%; Pred. No. 4.1e-32;
Matches 397; Conservative 0; Mismatches 315; Indels 15; Gaps 2;

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Qy 448 GCAGATCCAGGTTCTGGTAAACTATGCCCGTCTCGAAGAGGCTGAGAGGTCTCC 507
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 731 GAGGCGGCAATATTGTTCTTAAACGGTCGGAGTGAGATTA-----CGCCAGAACACGA 784
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Qy 508 AAAGAGATTGAAGCATCTGGTGGTGAAGCTATCACCTTCGGAGGAGATGTTTCAAAAGAA 567
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 785 CAGGAATTGAGCCCTTTGGGTAAATCTATTGGCCTTTCTGGAGATATTTCGATTTT 844
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 568 GCTGATGAGAGTCTATGATGAAAGCAGCTCTAGATAAATGGGGAACAATAGATGTCTG 627
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 845 GATCGGCGAGGTGAGATGATTCAGCAACAGTTGACCAATTAGGCTCGATTGATATTCTG 904
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Qy 628 GTAAATAATGAGGGATTACACGACACATTTGTTGATGAGATGAAGAAATCTCAGTGG 687
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Qy 905 GTGAATAACCTGGGATTACGAAATGACAAATTAATTATTACGAATGACAAAGAGGATTT 964
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Qy 688 CAAGACGTAAATTGATCTGAATCTTACTGGCGTCTTCCTTTTGACACAGGCTGCAACAAA 747
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Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 748 GTAATGATGAAAAAGAGAAAGGAAAAATTATCAACATTGCAATCTGTATGTTGCTTACT 807
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1025 CGTATGATGAACAACAGAGTGGTCCGATTATTAATATGCGCTAGCGTTTCTGGTTAATG 1084
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 808 GGCATGTTGGCCAGCTAAATTATAGCCAGCCAGGCTGGAGTGAATGGTTTCACAAA 867
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1085 GGAATGTTGGTCAAGCAAACTACGCTGCGAGTAAAGCGGFGTCGTTGGTTTACTAAA 1144
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 868 ACAGTTGCCAGGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCAACAGGGTTC 927
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1145 TCGGTGGCAGAGAGTTGGCGCGCGGTATTACCTGCAATGCGATTGCACCAGGGTTT 1204
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Qy 1265 ATTCCTTTACAAACGTTTGGGCAAGTCGAAGATGTCGAGCTACAGCGATTTTCTAGCT 1324
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Qy 1048 CTTAACCCCGCAGCTAGCTATATGCTGACAGAGGTGCTTTACAAATTGACGAGGAGTGTGA 1107
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Qy 1325 AAAAGTCC-----CTATATTACTGGGCAAGTCGTCAATGTCGATGCGGCGGTAGTC 1375
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Qy 1108 ATGTAAG 1114
Db      ||| ||| |||
Qy 1376 ATGCACG 1382
Db      ||| ||| |||

```

Search completed: November 7, 2003, 17:10:27
Job time : 450 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 13:17:29 ; Search time 3088 Seconds

(without alignments)
10436.443 Million cell updates/sec

Title: US-10-024-806-1

Perfect score: 1326

Sequence: 1 G9CGGAGCTTCCAGGCC.....aaaaaaaaaaaaaaaaaaaa 1326

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562794

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1326	100.0	1342	11 AY106146	AY106146 Zea mays
2	635	47.9	646	14 CB604782	CB604782 3529.1.61
3	615.2	46.4	639	13 BQ744718	BQ744718 946108E11
4	606	45.7	659	14 CD484893	CD484893 3529.1.11

C	5	598.4	45.1	600	10	BE510479	BE510479 946053B11
	6	598.4	45.1	648	13	BU098345	BU098345 946134D10
	7	585.6	44.2	626	10	BE510480	BE510480 946053B11
	8	584.6	44.1	637	13	BQ778788	BQ778788 946114C11
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	10	576.2	43.5	618	13	BQ779235	BQ779235 946117H09
	11	570.4	43.0	600	13	BQ293972	BQ293972 1091024F0
	12	550	41.5	557	13	BU092521	BU092521 946152D04
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	14	538.2	40.6	577	14	CA830470	CA830470 1117007C0
	15	533.8	40.3	539	13	BU092794	BU092794 946157G10
C	16	525.2	39.6	560	13	BU050646	BU050646 1111031D0
	17	524.8	39.6	530	13	BQ667989	BQ667989 946102E05
	18	511	38.5	553	12	BF543006	BF543006 949072A05
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	20	493.2	37.2	532	12	BM737474	BM737474 952056D06
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	22	483.6	36.5	490	12	BM953553	BM953553 952063F07
C	23	457	34.5	457	14	CD510389	CD510389 3529.1.11
	24	456.8	34.4	623	9	AV938005	AV938005 AV938005
	25	439.6	33.2	692	10	BF473272	BF473272 WHE0926.E
	26	438	33.0	640	9	AV913625	AV913625 AV913625
C	27	437.6	32.4	692	9	AV943057	AV943057 AV943057
	28	429.6	32.2	852	12	BM814438	BM814438 EST592532
	29	426.6	32.2	754	12	BM408233	BM408233 EST582560
	30	426.4	31.7	765	12	BM814281	BM814281 EST592374
	31	419.8	31.6	700	9	AL505428	AL505428 AL505428
	32	419.6	31.6	700	9	AL505428	AL505428 AL505428
	33	419.2	31.3	985	10	BE412873	BE412873 MCG006.B0
	34	415.2	31.3	985	10	BE412873	BE412873 MCG006.B0
	35	411.2	31.0	700	9	AL503431	AL503431 AL503431
C	36	406.8	30.7	418	13	BQ667988	BQ667988 946102E05
	37	403	30.4	585	14	CA012350	CA012350 HT05C23F
	38	401.6	30.3	677	9	AW311560	AW311560 sgfie09.Y
	39	387.6	29.2	802	10	BG417399	BG417399 HVSMEK001
	40	382.4	28.8	384	10	BE552632	BE552632 946082H02
C	41	380.6	28.7	677	9	AI622760	AI622760 486106D08
	42	368.4	27.8	494	14	CB966694	CB966694 NL41.H02
	43	367	27.7	610	13	BQ914905	BQ914905 QHB12105.
	44	366.6	27.6	589	10	BF484665	BF484665 WHE2318.C
	45	364	27.5	475	14	CB9666729	CB9666729 NL41.G11

ALIGNMENTS

RESULT 1	AY106146	AY106146	1342 bp	mrna	linear	HTC 16-OCT-2002
LOCUS	AY106146	Zea mays	PC0074795	mrna	sequence.	
DEFINITION	AY106146	Zea mays	PC0074795	mrna	sequence.	
ACCESSION	AY106146	Zea mays	PC0074795	mrna	sequence.	
VERSION	AY106146.1	GI:21209224				
KEYWORDS	HTC					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	1 (bases 1 to 1342)					
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 1342)					
AUTHORS	Coe, E.H.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the					

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES source

Location/Qualifiers

1. .1342

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="MaizeDB:634127"

/db_xref="taxon:4577"

/clone_lib="Maize Mapping Project/DuPont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for overgo addressing of BACs in conjunction with the M Mapping Project"

a 315 c 343 g 323 t

Query Match.	100.0%;	Score 1326;	DB 11;	Length 1342;
Best Local Similarity	100.0%;	Pred. No. 2.2e-126;		
Matches 1326;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GC	GGGAGCTTCCAAAGCCCGCTGCCCAATAGACTCCTCCCATACGTCCTCCCATCGTGTCTGTGCTCC	60
DB				
QY	17	GC	GGGAGCTTCCAAAGCCCGCTGCCCAATAGACTCCTCCCATACGTCCTCCCATCGTGTCTGTGCTCC	76
DB				
QY	61	GT	CACGGCTCAAATACTCCGGCTGCATCTCCAAAGCACACTGCTCCCTCTGGCTTCCCGC	120
DB				
QY	77	GT	CACGGCTCAAATACTCCGGCTGCATCTCCAAAGCACACTGCTCCCTCTGGCTTCCCGC	136
DB				
QY	121	CT	CCTCTTCGGCTCTTCGGCTCCGAGCCCGCTCATAGGCCACCGCCCGCCACACCGGA	180
DB				
QY	137	CT	CCTCTTCGGCTCTTCGGCTCCGAGCCCGCTCATAGGCCACCGCCCGCCACACCGGA	196
DB				
QY	181	GC	AGCAGCAGCAGTCTCTCTCCCGGCTGGCGTGGAGCAGCGGGGGCGCGCGCCCTCC	240
DB				
QY	197	GC	AGCAGCAGCAGTCTCTCTCCCGGCTGGCGTGGAGCAGCGGGGGCGCGCGCCCTCC	256
DB				
QY	241	CG	CGGGGGTTTGTCACGTTTGGTGGAGCGCCCGCCCGCTTCTCTCCACGCTGCGGTCC	300
DB				
QY	257	CG	CGGGGGTTTGTCACGTTTGGTGGAGCGCGCCCGCTTCTCTCCACGCTGCGGTCC	316
DB				
QY	301	GG	CGCTGGGTTCTCTGCTGTGCAACCCATCTGCTGCTGTGGACACAGCAGTTGTAAAA	360
DB				
QY	317	GG	CGCTGGGTTCTCTGCTGTGCAACCCATCTGCTGCTGTGGACACAGCAGTTGTAAAA	376
DB				
QY	361	GAT	GCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACAGTGCATCTPAGAGGANTTGGT	420
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QY	377	GAT	GCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACAGTGCATCTPAGAGGANTTGGT	436
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QY	421	AAG	CACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGTTCTGGTAAAACTATGCCCGG	480
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QY	437	AAG	CACTGCTCTAGCCCTTGGAAAGCAGGATGCAAGTTCTGGTAAAACTATGCCCGG	496
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QY	481	TC	CTCGAAAGAGGCTGGAAGGCTCTCCAAAGAGATTGAAGCATCTGGTGGTGAAGCTATC	540
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QY	497	TC	CTCGAAAGAGGCTGGAAGGCTCTCCAAAGAGATTGAAGCATCTGGTGGTGAAGCTATC	556
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QY	541	AC	CTTCGGAGAGATGTTTCAAAAGAGCTGATGTAGAGTCTATGATGAAAGCAGCTCTA	600
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QY	557	AC	CTTCGGAGAGATGTTTCAAAAGAGCTGATGTAGAGTCTATGATGAAAGCAGCTCTA	616
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QY	601	GATA	AATGGGGAACAATAGATGTCTGTTAAATTAATGCGGGAATTACAGAGACACATGT	660
DB				
QY	617	GATA	AATGGGGAACAATAGATGTCTGTTAAATTAATGCGGGAATTACAGAGACACATGT	676
DB				
QY	661	TT	GATGAGGATGAAGAAATCTCAGTGGCAGACGCTAATTGATCTGAATCTTACTGGCGTC	720
DB				
QY	677	TT	GATGAGGATGAAGAAATCTCAGTGGCAGACGCTAATTGATCTGAATCTTACTGGCGTC	736
DB				
QY	721	TT	CCTTTGTACACAGGCTGCAACAAAAGTATGATGAAAAAGAGAAAGGGAAAAATATC	780
DB				

Db	737	TTCTTTGTRCAGGCTGCAAAAAGTAATGATGAAAAGAAAGGAAAAATATC	796
Qy	781	AACATTGCATCTGTAGTTGGTCTTACTTGGCAATGTTGGCCAACTAATTATATGCGCAGCC	840
Db	797	AACATTGCATCTGTAGTTGGTCTTACTTGGCAATGTTGGCCAACTAATTATATGCGCAGCC	856
Qy	841	AAGCGTGGAGTATCGGTTTCACAAAAACAGTGGCCAGGAGTATCGAAGCAAAATATC	900
Db	857	AAGCGTGGAGTATCGGTTTCACAAAAACAGTGGCCAGGAGTATCGAAGCAAAATATC	916
Qy	901	AATGTGAATGCTATTGCACACGAGGTTCAATTGTCATCTGATATGACTCCGAACTTGGAGAA	960
Db	917	AATGTGAATGCTATTGCACACGAGGTTCAATTGTCATCTGATATGACTCCGAACTTGGAGAA	976
Qy	961	GAGCTTGAGAGAAAAATCTGTCAACCATTCCTGTAGGAGATATGGCCAAACAGAGGAA	1020
Db	977	GAGCTTGAGAGAAAAATCTGTCAACCATTCCTGTAGGAGATATGGCCAAACAGAGGAA	1036
Qy	1021	GTTGCAGGGTTGTCAGAGTTCCTGGCCCTTAACCCCGCAGCTAGCTATATGACTGACACAG	1080
Db	1037	GTTGCAGGGTTGTCAGAGTTCCTGGCCCTTAACCCCGCAGCTAGCTATATGACTGACACAG	1096
Qy	1081	GTGCTTACATTTGAACGGAGGATGGTAAGATTGAGTTAGTTAGCTTCGATCTTCTA	1140
Db	1097	GTGCTTACATTTGACGGAGGATGGTAAGATTGAGTTAGTTAGCTTCGATCTTCTA	1156
Qy	1141	CTTTTGCCTGAGCATTTAAAGTTTGAACACCCCTTGTGTGCACGGCGATTTTGGACAAACA	1200
Db	1157	CTTTTGCCTGAGCATTTAAAGTTTGAACACCCCTTGTGTGCACGGCGATTTTGGACAAACA	1216
Qy	1201	ATTAGTGTGTCTCTTTCTTTTGPAACTCTCTGGTAAATAAATCTAGCATGTGGATGGA	1260
Db	1217	ATTAGTGTGTCTCTCTTTCTTTTGPAACTCTCTGGTAAATAAATCTAGCATGTGGATGGA	1276
Qy	1261	AGTTTGAATCTGGTTTTTCGTGTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	1320
Db	1277	AGTTTGAATCTGGTTTTTCGTGTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	1336
Qy	1321	AAAAA 1326	
Db	1337	AAAAA 1342	

RESULT 2	
CB604782	
LOCUS	linear EST 16-MAY-2003
DEFINITION	3529_1_61_1_C02.y_1 3529 - 2 mm ear tissue from Schmidt and Hake
ACCESSION	CB604782
VERSION	labs-Zea mays cDNA, mRNA sequence.
KEYWORDS	CB604782.1 GI:29544402
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 646)
TITLE	Walbot.V.
JOURNAL	Maize ESTs from various cDNA libraries sequenced at Stanford University
COMMENT	Unpublished Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 3529_1_61_1 row: C column: 02. Location/Qualifiers 1..646 /organism="Zea mays"
FEATURES	
source	

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/note="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu amplified. Ampicillin is the selection marker."
BASE COUNT 136 a 191 c 178 g 141 t
ORIGIN
Query Match 47.9%; Score 635; DB 14; Length 646;
Best Local Similarity 99.8%; Pred. No. 5.6e-56;
Matches 646; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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DB 1 TCCCCCAATAGACTCTCCCATCCG-GCTTGCTCGCTCAGCGCTCAAAATACCCGCT 59
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QY 144 CCGAGCGCCCTCATGGCCAGCGCGCGCCGCGCCAGCAGCAGCAGCAGCAGCTCTCTCC 203
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QY 204 GGCTGCGGCTGGAGCAGCGCGCGCGCGCGCTCCGCGCGGGGTTTCGTCACGTTGG 263
DB 180 GGCTGCGGCTGGAGCAGCGCGCGCGCGCGCTCCGCGCGGGGTTTCGTCACGTTGG 239
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DB 240 TGGAGCGCCCGCGCGCTTCTCTCCACGCTGCGGTCGCGCGCTGCTCTGCTGTC 299
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DB 300 AACCAGCTGCTGCTGTTGAACAGCAGTGTGTAAGAGTCTTAAAGATCTACCAAGCTGGAAGCTCC 359
QY 384 AGTTGTTGTTGTTACAGTGATCTAGAGGATTTGTAAGCACTGCTCTAGCCCTTGG 443
DB 360 AGTTGTTGTTGTTACAGTGATCTAGAGGATTTGTAAGCACTGCTCTAGCCCTTGG 419
QY 444 AAAAGCAGATGCAAGGTTCTGTTAACTATGCGCGGTCCTCGAAAGGCTGAAGAGT 503
DB 420 AAAAGCAGATGCAAGGTTCTGTTAACTATGCGCGGTCCTCGAAAGGCTGAAGAGT 479
QY 504 CTCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATCACCTTCGAGGAGATGTTCAA 563
DB 480 CTCCAAAGAGATTGAAGCATCTGGTGTGAGGCTATCACCTTCGAGGAGATGTTCAA 539
QY 564 AGAAGCTGATGTAGAGTCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGT 623
DB 540 AGAAGCTGATGTAGAGTCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGT 599
QY 624 GCTGTAATAATGAGGATTTACAGAGACACATTTGTTGATGAGA 670
DB 600 GCTGTAATAATGAGGATTTACAGAGACACATTTGTTGATGAGA 646

RESULT 3
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LOCUS 946108E11.y1 946 - tassell primordium prepared by Schmidt lab Zea
DEFINITION mays cDNA, mRNA sequence.
ACCESSION BQ744718
VERSION BQ744718.1 GI:21891505
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 639)

AUTHORS Walbot, V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2927
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946108 row: E column: 11.
Location/Qualifiers
1. 639
/organism="Zea mays"
/mol_type="mRNA"
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/db_xref="taxon:4577"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to inflorescence development"
/lab_host="XL0LR"
/clone_lib="946 - tassell primordium prepared by Schmidt lab"
/note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridZAP. Sample insert size range was 350 bp to 3 kb with a 1 kb average."

BASE COUNT 168 a 138 c 180 g 153 t

Query Match 46.4%; Score 615.2; DB 13; Length 639;
Best Local Similarity 99.5%; Pred. No. 5.8e-54;
Matches 617; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 20 GCGGGGCGCGCGCGCTCCCGCGGGGTTCTCACGTTTGTGGAGCGCGCGCGC 79
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DB 80 TTCTCTCCACGCTGCGCGCTCGCGCGGGTTCTCTGCTGTGCAACCAATGTTGCTGCT 139
QY 340 GTTGAAACAAGCAGTTGTAAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 399
DB 140 GTTGAAACAAGCAGTTGTAAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 199
QY 400 GGTGCATCTAGAGGATTTGTAAGGCAACTGCTTAGCCCTTGAAGAAGCAGGATGCAAG 459
DB 200 GGTGCATCTAGAGGATTTGTAAGGCAACTGCTTAGCCCTTGAAGAAGCAGGATGCAAG 259
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DB 260 GTTCTGTGTAACATATGCGCGTCTCGAAAGAGCTCAAGAGGTTCTCAAGAGATTGAA 319
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QY 640 GGGATTCACGAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGCAGAGAGCTAATT 699
DB 440 GGGATTCACGAGACACATTTGTTGATGAGGATGAAGAAATCTCAGTGCAGAGAGCTAATT 499
QY 700 GATCTGAATCTTACTGGCGCTCTTCCTTTGTACACAGGCTGCACAAAGTAATGATGAA 759

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500 GATCTGAATCTTACTGGTGTCTTCTCTTGTCACAGGCTGCAACAAAGTAATGANGAAA 559
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760 AAGAGAAAGGAAAAAATATCAACATTCATCTGTAGTTGGTCTTACTGGCAATGTTGGC 819
|||||
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820 CAAGCTAATTTAGCGCAGC 839
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RESULT 4
CD484893/c
LOCUS CD484893 659 bp mRNA linear EST 04-JUN-2003
DEFINITION 3529_1_110_1_C12.x.1 3529 - 2 mm ear tissue from Schmidt and Hake
labs Zea mays cDNA, mRNA sequence.
ACCESSION CD484893
VERSION CD484893.1 GI:31406161
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 659)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3529_1_110_1 row: C column: 12.
Location/Qualifiers
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/cultivar="B73"
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labs"
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Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu
amplified. Ampicillin is the selection marker."
BASE COUNT 183 a 169 c 116 g 191 t
ORIGIN

Query Match 45.7%; Score 606; DB 14; Length 659;
Best Local Similarity 98.5%; Pred. No. 4.9e-53;
Matches 654; Conservative 0; Mismatches 5; Indels 5; Gaps 4;

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628 GTAATATATGCGGATTTACGAGACACATTTGATGAGATGAAGAAATCTCAGTGG 687
599 GTAATATATGCGGATTTACGAGACACATTTGATGAGATGAAGAAATCTCAGTGG 540
688 CAAGACGTAATGATCTGAATCTTACTGGCTCTTCTTGTACACAGCTGCAACAAA 747
539 CAAGACGTAATGATCTGAATCTTACTGGCGCTTCTTGTACACAGCTGCAACAAA 480
748 GTAATGATGAAGAAAGGAAAAAATATCAACATTCATCTGTAGTTGGTCTTACT 807
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Db 479 GTATATGTAAGAAAGAGAAAGGAAAAAATATCAACATTCGATCTGTAGTTGGTCTTACT 420
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Db 419 GGCAATGTTGGCCCAAGCTAATTTATAGCGCAGCCCAAGGCTGGAGTGAATGGTTTTCACAAA 360
Qy 868 ACAGTTGCCAGGAGATGCAAGCAGAAATATCAATGTGAATGCTATTCACACAGGTTTC 927
Db 359 ACAGTTGCCAGGAGATGCAAGCAGAAATATCAATGTGAATGCTATTCACACAGGTTTC 300
Qy 928 ATTGCATCTGATATGACTGCCGAACCTTGGAGAGAGAGCTTGGAGAGAAATCTTCTCAACC 987
Db 299 ATTGCATCTGATATGACTGCCGAACCTTGGAGAGAGAGCTTGGAGAGAAATCTTCTCAACC 240
Qy 988 ATTCCGTTAGGAGATATGCCCAACCCAGAGAGAGTTGCAGGGTTGGTGCAGTTCTCTGGCC 1047
Db 239 ATTCCGTTAGGAGATATGCCCAACCCAGAGAGAGTTGCAGGGTTGGTGCAGTTCTCTGGCC 180
Qy 1048 CTTAACCCCGCAGCTAGCTATATGACTGGACAGAGCTTGCAGGGTTGGTGCAGTTCTCTGGCC 1167
Db 179 CTTAACCCCGCAGCTAGCTATATGACTGGACAGAGCTTGCAGGGTTGGTGCAGTTCTCTGGTA 120
Qy 1108 ATGTAAGATTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTT 1167
Db 119 ATGTAAGATTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTTGAGTT 62
Qy 1168 CCCTGTTGTGCAAGCGGCGAATTTGGACAAACAATTAAGTTGTTCTCTTTTGTAAATA 1227
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Qy 1228 CTCT 1231
Db 4 CTCT 1

RESULT 5
BE510479/c
LOCUS BE510479 600 bp mRNA linear EST 07-AUG-2000
DEFINITION 946053B11.xl 946 - tassell primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION BE510479
VERSION BE510479.1 GI:9731727
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 600)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946053 row: B column: 11.
Location/Qualifiers
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lab"
FEATURES
source

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/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 KB with a 1 Kb average."
172 a 148 c 105 g 175 t
BASE COUNT

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Best Local Similarity	99.8%	Pred. No. 3.1e-52		
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Db	600	ACACATTTGTTGATGAGGATGAAGAAATCTCAGTGCAGCAAGCTGAATTTGATCTGAATCTTATA	541	
QY	713	CTGCGCTTCTCTTTGTACACAGGCTGCACAAAGAATGATGAAAAAGAGAAAGGGAA	772	
Db	540	CTGCTGCTCTCTTTGTACACAGGCTGCACAAAGAATGATGAAAAAGAGAAAGGGAA	481	
QY	773	AAATTATACAAATTCGATCTGTAGTTGGTCTTACTGCGCAATGTTGGCCCAAGCTTAATTATA	832	
Db	480	AAATTATCAACATTCGATCTGTAGTTGGTCTTACTGCGCAATGTTGGCCCAAGCTTAATTATA	421	
QY	833	CGCAGGCAAGGCTGGAGTGAATTCGGTTTCACAAAAACAGTTGCCAGGGAGTATGCAAGCA	892	
Db	420	CGCAGGCAAGGCTGGAGTGAATTCGGTTTCACAAAAACAGTTGCCAGGGAGTATGCAAGCA	361	
QY	893	GAAATATCAATGTGAATGCTATTGCAACAGGTTTCATTCGATCTGATATGACTGCCGAAC	952	
Db	360	GAAATATCAATGTGAATGCTATTGCAACAGGTTTCATTCGATCTGATATGACTGCCGAAC	301	
QY	953	TTGCGAAGAGCTTGAGAAAGAAATCTTGTCACACCATTCGGTTAGGAGGATATGGCCCAAC	1012	
Db	300	TTGCGAAGAGCTTGAGAAAGAAATCTTGTCACACCATTCGGTTAGGAGGATATGGCCCAAC	241	
QY	1013	CAGAGGAAGTTGCAGGGTTGCTCGAGTTTCCTGGCCCTTAACCCCGCAGCTAGCTATATGA	1072	
Db	240	CAGAGGAAGTTGCAGGGTTGCTCGAGTTTCCTGGCCCTTAACCCCGCAGCTAGCTATATGA	181	
QY	1073	CTGCAACAGGTGCTTACAATTGACCGAGGGATGGTAATGTAAGATTTGAGTTAGCTTGATG	1132	
Db	180	CTGCAACAGGTGCTTACAATTGACCGAGGGATGGTAATGTAAGATTTGAGTTAGCTTGATG	121	
QY	1133	CACCTTCTACTTTTGTCTGAGCAATTTAATGTTGAAACACCCCTTGTCTGCAACGGCGGATTTTG	1192	
Db	120	CACCTTCTACTTTTGTCTGAGCAATTTAATGTTGAAACACCCCTTGTCTGCAACGGCGGATTTTG	61	
QY	1193	GACACAAATAGTGTGTCTCTTCTTTTGTGTAATCTCTCTGGTAAATAAATCTAGCAATG	1252	
Db	60	GACACAAATAGTGTGTCTCTTCTTTTGTGTAATCTCTCTGGTAAATAAATCTAGCAATG	1	

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LOCUS	BU098345				
DEFINITION	9461134D10.y1.945 - tassell primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.				
ACCESSION	BU098345				
VERSION	BU098345.1	GI:22545986			
KEYWORDS	EST.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 648)				
AUTHORS	Walbot, V.				
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University				
JOURNAL	Unpublished				
COMMENT	Contact: Walbot V				
	Department of Biological Sciences				

Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946134 row: D column: 10

FEATURES	source	Location/Qualifiers
BASE COUNT	164 a	159 c 184 g 141 t
ORIGIN		lab"
		/note="Organ: tassels; Vector: HybrizAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between imm and 3mm. Sharon Stanfield prepared the cdna library in HybrizAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
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		Location/Qualifiers
Query Match	45.1%;	Score 598.4; DB 13; Length 648;
Best Local Similarity	97.4%;	Pred. No. 3e-52;
Matches 631;	Conservative 0;	Mismatches 11; Indels 6; Gaps 2;
QY	138	CGCGTCCGAGCGCCCTCATGTGCGCCACCGCGCGCCACCGCAGCAGCAGCAGCTCTC 197
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QY	198	CTCCCGCGTGCCTGTGAGCAGCAGCGCGCGCGCGCGCTCCCGCGGGGTTCGTCAC 257
Db	64	CTCCCGCGTGCCT--CAGCGCGCGGGCGCGCGCGCTCCCGCGGGGTTCGTCAC 120
QY	258	GTTTGTGTGAGGCGCGCGCGCTTCTCCACGCTGCGGTCCGGCGGTGGGTTCCTGTGG 317
Db	121	GTTTGTGTGAGGCGCGCGCGCTTCTCCACGCTGCGGTCCGGCGGTGGGTTCCTGTGG 180
QY	318	TGTGCAAAACCCATGTTGCTGTCTTCGAAACAGCAGTTGTAAAGATGCTACCAAGCTGGA 377
Db	181	TGTGCAAAACCCATGTTGCTGTCTTCGAAACAGCAGTTGTAAAGATGCTACCAAGCTGGA 240
QY	378	AGCTCCAGTTGTTGTTGTTTACAGGTGCATCTAGAGGATTTGTAAGCACTGCTCTAGC 437
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QY	438	CCTTGGAAAAGCAGGATGCAAGTTCTGTGTAACATATGCCCGTCTCTGAAAGAGGCTGA 497
Db	301	CCTTGGAAAAGCAGGATGCAAGTTCTGTGTAACATATGCCCGTCTCTGAAAGAGGCTGA 360
QY	498	AGAGGTCTCCAAAGACATGGAAGCATCTGGTGTGAGGCTATCACCTTCGAGGAGATGT 557
Db	361	AGAGGTCTCCAAAGACATGGAAGCATCTGGTGTGAGGCTATCACCTTCGAGGAGATGT 420
QY	558	TTCAAAGAAGCTGATGTAGAGCTTAGATGAAGCAGCTCTAGATAAATGGGGAACAAT 617
Db	421	TTCAAAGAAGCTGATGTAGAGCTTAGATGAAGCAGCTCTAGATAAATGGGGAACAAT 480
QY	618	AGATGTGCTGTTAAATAATGACGGGATTCACAGACACATGTTGATGAGGTGAAGA 677
Db	481	AGATGTGCTGTTAAATAATGACGGGATTCACAGACACATGTTGATGAGGTGAAGA 540
QY	678	ATCTCAGTGCACAGCAGTAATTCATCTGAATCTTACTGGCGTCTCTCTTTGTACAGGC 737
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QY	738	TGCACAAAAGTAAATGATGAAAAAGAAAGGAAAAATTTATCAACAT 785
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RESULT 7
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DEFINITION
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  946053B11.y1 946 - tassell primordium prepared by Schmidt lab Zea
  mays cDNA, mRNA sequence.
ACCESSION
  BE510480
VERSION
  BE510480.1 GI:9731728
KEYWORDS
  EST.
SOURCE
  Zea mays
ORGANISM
  Zea mays
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  1 (bases 1 to 626)
AUTHORS
  Walbot,V.
TITLE
  Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL
  Unpublished
COMMENT
  Contact: Walbot V
  Department of Biological Sciences
  Stanford University
  855 California Ave, Palo Alto, CA 94304, USA
  Tel: 650 725 8221
  Fax: 650 725 8221
  Email: walbot@stanford.edu
  Plate: 946053 row: B column: 11.
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        lab"
        /note="Organ: tassels; Vector: HybrizAP; Site 1: EcoRI;
        Site 2: XhoI; George Chuck dissected immature tassels
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        to 3 Kb with a 1 Kb average."
BASE COUNT
  136 a 169 c 175 g 146 t
ORIGIN
  101 TGCTCCCTCTGGCTTCCGCGCTCTCTTCGGGTCTCTCGCGTCCCGAGCGCCCTCATGG 160
  1 TGCTCCCTCTGGCTTCCGCGCTCTCTTCGGGTCTCTCGCGTCCCGAGCGCCCTCATGG 60
  161 CCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 220
  61 CCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 114
  221 CCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 280
  115 CCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 174
  281 TCTCTCCACAGCTGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 340
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  401 GTGCATCTAGAGGGATTGGTAGGCACTGCTCTAGCCCTTGGAAGAACAGGATCGAAG 460

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  RESULT 8
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  DEFINITION
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    946114C11.y1 946 - tassell primordium prepared by Schmidt lab Zea
    mays cDNA, mRNA sequence.
  ACCESSION
    BQ778788
  VERSION
    BQ778788.1 GI:21987260
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  SOURCE
    Zea mays
  ORGANISM
    Zea mays
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Zea.
  REFERENCE
    1 (bases 1 to 637)
  AUTHORS
    Walbot,V.
  TITLE
    Maize ESTs from various cDNA libraries sequenced at Stanford
  JOURNAL
    Unpublished
  COMMENT
    Contact: Walbot V
    Department of Biological Sciences
    Stanford University
    855 California Ave, Palo Alto, CA 94304, USA
    Tel: 650 723 2227
    Fax: 650 725 8221
    Email: walbot@stanford.edu
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        lab"
        /note="Organ: tassels; Vector: HybrizAP; Site 1: EcoRI;
        Site 2: XhoI; George Chuck dissected immature tassels
        between 1mm and 3mm. Sharon Stanfield prepared the cDNA
        library in HybrizAP. Sample insert size range was 350 bp
        to 3 Kb with a 1 Kb average."
BASE COUNT
  140 a 177 c 177 g 143 t
ORIGIN
  Query Match 44.1%; Score 584.6; DB 13; Length 637;
  Best Local Similarity 97.5%; Pred. No. 7.5e-51;
  Matches 627; Conservative 0; Mismatches 9; Indels 7; Gaps 3;

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74 TACTCCGCTGCATCTCCAAAGACACATGCTCCCTCTGGCTTCCCGCTCTCTCCGGCT 133
Db 1 TACTCCGCTGCATCTCC-AAGACACATGCTCCCTCTGGCTTCCCGCTCTCTCCGGCT 59
134 CTTTCCGCTCCGACGCTCCCTCATGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCG 193
Db 60 CTTTCCGCTCCGACGCTCCCTCATGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCG 116
194 TCTCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 253
Db 117 TCTCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCG 173
254 TCAGTTTGTGGAGGCGCGCGCTCTCTCCACGCTCCGCTCCGCTCCGCTCCGCTCCGCT 313
Db 174 TCAGTTTGTGGAGGCGCGCGCTCTCTCTCCACGCTCCGCTCCGCTCCGCTCCGCTCCG 233
314 CTGTGTGCACCAACCCATGTTGCTCTCTGTTGAACAGCAGTTGTAAGAGATGCTACCAAGC 373
Db 234 CTGTGTGCACCAACCCATGTTGCTCTCTGTTGAACAGCAGTTGTAAGAGATGCTACCAAGC 293
374 TGAAGCTCCAGTTGTTGTTTACAGTGCACTCTAGAGGATGTTGAAGCACTCTCTC 433
Db 294 TGAAGCTCCAGTTGTTGTTTACAGTGCACTCTAGAGGATGTTGAAGCACTCTCTC 353
434 TAGCCCTTGAAGAGCAGGATGCAAGGTTCTGTGTAACACTATGCCGCTCCGAGGAG 493
Db 354 TAGCCCTTGAAGAGCAGGATGCAAGGTTCTGTGTAACACTATGCCGCTCCGAGGAG 413
494 CTGAAGAGGCTCTCCAAAGAGATGAAGCATCTGTGTGTGAGGCTATCACCTTCCGAGGAG 553
Db 414 CTGAAGAGGCTCTCCAAAGAGATGAAGCATCTGTGTGTGAGGCTATCACCTTCCGAGGAG 473
554 ATGTTTCAAAGAGCAGTATGAGTCTATGATGAAGAGCAGCTCTAGTAATATGGGAA 613
Db 474 ATGTTTCAAAGAGCAGTATGAGTCTATGATGAAGAGCAGCTCTAGTAATATGGGAA 533
614 CAATAGATGCTCTGTAATTAATCAGGATTAACAGGATTAACAGGATTAACAGGATTA 673
Db 534 CAATAGATGCTCTGTAATTAATCAGGATTAACAGGATTAACAGGATTAACAGGATTA 593
674 AGAATCTCAGTGCACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATG 716
Db 594 AGAATCTCAGTGCACAGCAGTATGATGATGATGATGATGATGATGATGATGATGATG 636

RESULT 9

BQ778787/c

LOCUS

DEFINITION 946114C11.x1 946 - tassell primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.

ACCESSION

VERSION

BQ778787.1

GI:21987259

EST.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL

COMMENT

Contact: Walbot V

Department of Biological Sciences

Stanford University

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Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 946114 row: C column: 11.

FEATURES

Location/Qualifiers

source

1. 624

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="OH43"

/db_xref="taxon:4577"

/issue_type="tassels"

/dev_stage="just after the transition from vegetative to

inflorescence development"

/lab_host="XLOLR"

/clone_lib="946 - tassell primordium prepared by Schmidt

lab"

/notes="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;

Site 2: XhoI; George Chuck dissected immature tassels

between 1mm and 3mm. Sharon Stanfield prepared the cDNA

library in HybriZAP. Sample insert size range was 350 bp

to 3 Kb with a 1 Kb average."

BASE COUNT 175 a 153 c 121 g 175 t

ORIGIN

Query Match 44.0%; Score 583.4; DB 13; Length 624;

Best Local Similarity 97.3%; Pred. No. 1e-50;

Matches 604; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

Qy 682 CAGTGCACAGCAGTATGATCTGAATCTTACTGGGCTCTTCTTGTACACAGGCTGCA 741

Db 624 CAGTGCACAGCAGTATGATCTGAATCTTACTGGGCTCTTCTTGTACACAGGCTGCA 565

Qy 742 ACAAAGTATGATGAAAAAGAGAAAGGAAATATCAACATTCATCTGTAGTTGGT 801

Db 564 ACAAAGTATGATGAAAAAGAGAAAGGAAATATCAACATTCATCTGTAGTTGGT 505

Qy 802 CTTACTGGCAATGTCGGCAGCTAATATAGCGCAGCAGGCTGGAGTGGTTTC 861

Db 504 CTTACTGGCAATGTCGGCAGCTAATATAGCGCAGCAGGCTGGAGTGGTTTC 445

Qy 862 ACAAACAGTTCGCCAGGAGTATCAAGCAGAAATATCAATGTGAATGCTATTCACCA 921

Db 444 ACAAACAGTTCGCCAGGAGTATCAAGCAGAAATATCAATGTGAATGCTATTCACCA 385

Qy 922 GGTTTCATTCATCTGATATGACTGCGAACTTTGGAGAGAGCTTGAGAGAAATCTTG 981

Db 384 GGTTTCATTCATCTGATATGACTGCGAACTTTGGAGAGAGCTTGAGAGAAATCTTG 325

Qy 982 TCAACCATTCCTGTAGGAGATATGCCACAGAGAGAGCTTCAGGTTGGTCGATTC 1041

Db 324 TCAACCATTCCTGTAGGAGATATGCCACAGAGAGAGCTTCAGGTTGGTCGATTC 265

Qy 1042 CTGGCCCTTAAACCCCGCAGCTATATGACTGGACAGGCTTACAATTCACGAGGG 1101

Db 264 CTGGCCCTTAAACCCCGCAGCTATATGACTGGACAGGCTTACAATTCACGAGGG 205

Qy 1102 ATGTTAATGTAAGTATGAGTTAGTTAGTTCATCTTACTTTGTGAGCATTAATGT 1161

Db 204 ATGTTAATGTAAGTATGAGTTAGTTAGTTCATCTTACTTTGTGAGCATTAATGT 145

Qy 1162 TGAACACCTTGTGTGTCACGGCGATTTTGGACAAATATAGTGTCTCTTCTTT 1221

Db 144 TGAACACCTTGTGTGTCACGGCGATTTTGGACAAATATAGTGTCTCTTCTTT 85

Qy 1222 GTAATATCTCTCTGTAATAATCTAG-CATGTGGAATGGAATGGAATCTGGGTTTCG 1280

Db 84 GTAATATCTCTCTGTAATAATCTAGCCATGGAATGGAATGGAATCTGGGTTTCG 25

Qy 1281 TGTAAAAAATAAAAAA 1301

Db 24 TGTAAAAAATAAAAAA 4

RESULT 10

BQ779235

LOCUS

DEFINITION

946117H09.v1 946 - tassell primordium prepared by Schmidt lab Zea

mays cDNA, mRNA sequence.

618 bp mRNA linear

EST 26-JUL-2002

BQ779235

LOCUS


```

ACCESSION   BQ779235
VERSION     BQ779235.1  GI:21987707
KEYWORDS    Zea mays
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 618)
AUTHORS    Walbot,V.
TITLE      Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL     Unpublished
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946117 row: H column: 09.
FEATURES    Source
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            /mol_type="mRNA"
            /cultivar="OH43"
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            /tissue_type="tassels"
            /dev_stage="just after the transition from vegetative to
            inflorescence development"
            /lab_host="XL0LR"
            /clone_lib="946 - tassels primordium prepared by Schmidt
            lab"
            /note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
            Site 2: XhoI; George Chuck dissected immature tassels
            between 1mm and 3mm. Sharon Stanfield prepared the cDNA
            library in HybriZAP. Sample insert size range was 350 bp
            to 3 Kb with a 1 Kb average."
BASE COUNT  180 a 108 c 159 g 170 t 1 others
ORIGIN
Query Match 43.5%; Score 576.2; DB 13; Length 618;
Best Local Similarity 99.0%; Pred. No. 5.5e-50;
Matches 600; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
Qy 657 ATTGTTGATGAGGATGAAGAATCTCAGTGGCAAGACGTAATTGATCTGAATCTTACTGG 716
Db 15 ACTGTTGATGAGGATGAAGAATCTCAG-GGCNAGACGTAATTGATCTGAATCTTACTGG 73
Qy 717 CGTCTTCCTTTGTACACAGGCTGCACAAAAGTAATGATGAAGAAGAGAAAGGAAAAAT 776
Db 74 -GTCTTCCTTTGTACACAGGCTGCACAAAAGTAATGATGAAGAAGAGAAAGGAAAAAT 132
Qy 777 TATCAACATTGCATCTGATGTTGGTCTTACTGGCAATGTTGCCAAGCTAATTATAGCGC 836
Db 133 TATCAACATTGCACTGATGTTGGTCTTACTGGCAATGTTGCCAAGCTAATTATAGCGC 192
Qy 837 AGCCAAGCTGGAGTGATGTTGTTTCACAAAACAGTTCGCCAGGAGTATGCAAGCAGAAA 896
Db 193 AGCCAAGCTGGAGTGATGTTGTTTCACAAAACAGTTCGCCAGGAGTATGCAAGCAGAAA 252
Qy 897 TATCAATGTGAATGCTATATGACCAAGGTTCTATTCATCTGATATGATGCGCAACTGG 956
Db 253 TATCAATGTGAATGCTATATGACCAAGGTTCTATTCATCTGATATGATGCGCAACTGG 312
Qy 957 AGAAGAGCTTGAGAGAAAATCTTCTCAACCAATCCGTTAGGAGATATGCCCAACAGAA 1016
Db 313 AGAAGAGCTTGAGAGAAAATCTTCTCAACCAATCCGTTAGGAGATATGCCCAACAGAA 372
Qy 1017 GGAAGTTGAGGTTGGTCGAGTTCCTTGGCCCTTAACCCCGCAGCTAGCTATATGACTGG 1076
Db 373 GGAAGTTGAGGTTGGTCGAGTTCCTTGGCCCTTAACCCCGCAGCTAGCTATATGACTGG 432

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QY 1077 ACAGGTGCTTACAATTGACGGAGGGATGTAATGTAAGATTGAGTTAGCTTATGATCACT 1136
DB 433 ACAGGTGCTTACAATTGACGGAGGGATGTAATGTAAGATTGAGTTAGCTTATGATCACT 492
QY 1137 TCTACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTGCACGGGCGAATTTGGACA 1196
DB 493 TCTACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTGCACGGGCGAATTTGGACA 552
QY 1197 ACAAAATTAGTGTCTCTCTTTCTTTGTAATACTCTCTGTTAATAAATCTAGCATGTGGAA 1256
DB 553 ACAAAATTAGTGTCTCTCTTTCTTTGTAATACTCTCTGTTAATAAATCTAGCATGTGGAA 612
QY 1257 TGGAG 1262
DB 613 TGGAG 618

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RESULT 11
BQ293972
LOCUS     BQ293972
DEFINITION 600 bp mRNA linear EST 15-MAY-2002
            Schmidt lab Zea mays cDNA, mRNA sequence.
ACCESSION BQ293972.1  GI:20802922
VERSION   BQ293972
KEYWORDS  EST.
SOURCE    Zea mays
ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 600)
AUTHORS   Walbot,V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL   Unpublished
COMMENT   Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1091024 row: E column: 01.
FEATURES  Source
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            /organism="Zea mays"
            /mol_type="mRNA"
            /cultivar="OH43"
            /db_xref="taxon:4577"
            /tissue_type="Inflorescence meristem - floral organ
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            /dev_stage="0.5 cm to 2 cm"
            /lab_host="Stratagene XL0LR"
            /clone_lib="1091 - Immature ear with common ESTs screened
            by Schmidt lab"
            /note="Organ: Immature ear; Vector: PAD-GAL4; Site 1:
            EcoRI; Site 2: XhoI; RNA from library 606 was filtered for
            common ESTs found in 606."
BASE COUNT 186 a 104 c 144 g 166 t
ORIGIN
Query Match 43.0%; Score 570.4; DB 13; Length 600;
Best Local Similarity 99.8%; Pred. No. 2.2e-49;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 697 ATTGATCTGAATCTTACTGGCGTCTTCTTTGTACACAGCTGCAACAAAAGTAATCATG 756
DB 1 ATTGATCTGAATCTTACTTGTCTTCTTGTACAGGCTGCAACAAAAGTAATCATG 60
QY 757 AAAAAGAGAAAGGAAAAAATATCAACATTGCTAGTCTTCTTCTTCTTCTTCTTCTTCTT 816
DB 61 AAAAAGAGAAAGGAAAAAATATCAACATTGCTAGTCTTCTTCTTCTTCTTCTTCTTCTT 120

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817 GGCCAGCTAATTATAGCGCAGCAGGCTGGAGTGATGGTTTCAAAAACAGTTGCC 876
 121 GGCCAGCTAATTATAGCGCAGCAGGCTGGAGTGATGGTTTCAAAAACAGTTGCC 180
 877 AGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCAACAGGTTTCAATGCACT 936
 181 AGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCAACAGGTTTCAATGCACT 240
 937 GATATGCTGCGCACTTTGAGAGAGAGCTTGAGAGAAATCTTGTGCAACATTCGGTTA 996
 241 GATATGCTGCGCACTTTGAGAGAGAGCTTGAGAGAAATCTTGTGCAACATTCGGTTA 300
 997 GGGAGATATGCCAACAGAGAGAGTTGCGAGGTTGTCGAGTTCTGGCCCTTAACCCC 1056
 301 GGGAGATATGCCAACAGAGAGAGTTGCGAGGTTGTCGAGTTCTGGCCCTTAACCCC 360
 1057 GCAGTAGCTATATGACTGGACAGAGTCTTACAATTTGACGAGGAGTGTGAATGAAGAT 1116
 361 GCAGTAGCTATATGACTGGACAGAGTCTTACAATTTGACGAGGAGTGTGAATGAAGAT 420
 1117 TTGAGTAGCTGATGACATCTCTTCTGCTGAGCAATTTAATGTTGAAACACCTTGTG 1176
 421 TTGAGTAGCTGATGACATCTCTTCTGCTGAGCAATTTAATGTTGAAACACCTTGTG 480
 1177 TGCAAGGCGGATTTTGACACAAATAGTGTCTCTCTTCTTGTGAATCTCTCTGCT 1236
 481 TGCAAGGCGGATTTTGACACAAATAGTGTCTCTCTTCTTGTGAATCTCTCTGCT 1296
 1237 AATAAATCTAGCATGTGGAATGGAATTTGAAA 1268
 541 AATAAATCTAGCATGTGGAATGGAATTTGAAA 572

RESULT 12

BU092521
 LOCUS 946152D04.y1 946 - tassels primordium prepared by Schmidt lab Zea
 DEFINITION mays cDNA, mRNA sequence.

ACCESSION BU092521
 VERSION BU092521.1 GI:22542083

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 557)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University

COMMENT Unpublished

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 946152 row: D column: 04.

FEATURES

source

1. 557

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="OH43"

/db_xref="taxon:4577"

/tissue_type="tassels"

/dev_stage="just after the transition from vegetative to inflorescence development"

/lab_host="XLOLR"

/clone_lib="946" - tassels primordium prepared by Schmidt lab

/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels"

between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

BASE COUNT 168 a 96 c 137 g 156 t

ORIGIN

Query Match 41.5%; Score 550; DB 13; Length 557;

Best local similarity 100.0%; Pred. No. 2.7e-47;

Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 719 TCTTCTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTA 778

DB 1 TCTTCTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTA 60

QY 779 TCAACATTTGATCTGTAGTTGGTCTTTACTGCGCAATTTGTCGCCAAGCTTAATATAGCGCAG 838

DB 61 TCAACATTTGATCTGTAGTTGGTCTTTACTGCGCAATTTGTCGCCAAGCTTAATATAGCGCAG 120

QY 839 CCAAGGCTGGAGTGATTTGCACAAAACAGTTGCCAGGAGTATGCAAGCAAGAATA 898

DB 121 CCAAGGCTGGAGTGATTTGCACAAAACAGTTGCCAGGAGTATGCAAGCAAGAATA 180

QY 899 TCAATGTGAATGCTATTGCAACAGGTTTCAATGCTCATCTGATATCACTGCCCACTTGGAG 958

DB 181 TCAATGTGAATGCTATTGCAACAGGTTTCAATGCTCATCTGATATCACTGCCCACTTGGAG 240

QY 959 AAGAGCTTTGAGAGAAATCTTGTCAACCAATTCGGTTAGGAGATATGCGCAACCGAGG 1018

DB 241 AAGAGCTTTGAGAGAAATCTTGTCAACCAATTCGGTTAGGAGATATGCGCAACCGAGG 300

QY 1019 AAGTTGCGAGGTTGTCGAGTTCTGCGCCCTTAACCCGCGAGTATGCTATATGACTGGAC 1078

DB 301 AAGTTGCGAGGTTGTCGAGTTCTGCGCCCTTAACCCGCGAGTATGCTATATGACTGGAC 360

QY 1079 AGTGCTTTACAATTGACGAGGATGTAATGTAAGATTGTAGTTAGCTTGTGCACTTC 1138

DB 361 AGTGCTTTACAATTGACGAGGATGTAATGTAAGATTGTAGTTAGCTTGTGCACTTC 420

QY 1139 TACTTTTGTGAGCAATTTAATGTAACACCCCTTGTGTGTCACGGCGATTTTGGACAAC 1198

DB 421 TACTTTTGTGAGCAATTTAATGTAACACCCCTTGTGTGTCACGGCGATTTTGGACAAC 480

QY 1199 AATATGATGTTGCTCTCTCTTCTTTGTAATCTCTCTGTAATAATCTAGCATGTGGAATG 1258

DB 481 AATATGATGTTGCTCTCTTCTTTGTAATCTCTCTGTAATAATCTAGCATGTGGAATG 540

QY 1259 GAAGTTGAAA 1268

DB 541 GAAGTTGAAA 550

RESULT 13

BM737475/c

LOCUS BM737475

DEFINITION 952056D06.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea

ACCESSION BM737475

VERSION BM737475.1

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 589)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL University

COMMENT Unpublished

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 952056 row: D column: 06.

FEATURES
source
1. 589
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/tissue type="suspension culture"
/dev stage="mixed logarithmic and stationary growth phases"
/lab_host="DH10B"
/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

BASE COUNT 131 a 170 c 144 g 144 t
ORIGIN

Query Match 41.2%; Score 545.8; DB 12; Length 589;
Best Local Similarity 97.4%; Pred. No. 6.9e-47;
Matches 566; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

Qy 168 GCGGCCACCGCAGCAGCAGCAGTCTCTCCCGGCTCGGTGGAGCAGCGGGGC 227
Db 589 GCGCGCCACCGCAGCAGCAGTCTCTCCCGGCTCGGTGGAGCAGCGGGGC 533
Qy 228 GCGCGCCCTCCCGCGGGGTTCGTACGTTGGTGGAGCGCGCCCTCTCTCC 287
Db 532 GCGCGCCCTCCCGCGGGGTTCGTACGTTGGTGGAGCGCGCCCTCTCTCC 473
Qy 288 CACGCTGGGTCCGCGCGGTTCCTGTGTGCAACCCATGTTGCTGTGAACA 347
Db 472 CACGCTGGGTCCGCGCGGTTCCTGTGTGCAACCCATGTTGCTGTGAACA 413
Qy 348 AGCAATTGTAAGAATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTACAGGTGCATC 407
Db 412 AGCAATTGTAAGAATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTACAGGTGCATC 353
Qy 408 TAGAGGATTTGGTAGGCACTGCTAGCCCTTGGAAAGCAGGATCGAGTTCTGGT 467
Db 352 TAGAGGATTTGGTAGGCACTGCTAGCCCTTGGAAAGCAGGATCGAGTTCTGGT 293
Qy 468 AAATATGCGCGTCTCCGAAAGAGGCTCAAGAGTCTCCAAAGAGATTGAAGCATCTGG 527
Db 232 AAATATGCGCGTCTCCGAAAGAGGCTCAAGAGTCTCCAAAGAGATTGAAGCATCTGG 233
Qy 528 TGGTAGGCTATCACTTCGAGGAGATGTTTCAAAAGAGCTGATGATGAT 587
Db 232 TGGTAGGCTATCACTTCGAGGAGATGTTTCAAAAGAGCTGATGATGAT 173
Qy 588 GAAAGCAGCTTAGATAATGGGAACAATAGATGCTGTTAATAATGCGGATAC 647
Db 172 GAAAGCAGCTTAGATAATGGGAACAATAGATGCTGTTAATAATGCGGATAC 113
Qy 648 AGCAGACATTTGTTGATGAGATCAAGAAATCTCAGTGGCAGACGTAATTGATCGAA 707
Db 112 AGCAGACATTTGTTGATGAGATCAAGAAATCTCAGTGGCAGACGTAATTGATCGAA 53
Qy 708 TCTTACTGGCGTCTTCCTTTGATACAGGCTGCAACAAAAG 748
Db 52 TCTTACTGGCGTCTTCCTTTGATACAGGCTGCAACAAAAG 12

RESULT 14

CA830470

LOCUS

DEFINITION

CA830470.1

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 577

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="taxon:4577"

/clone_lib="1117 - Unigene V from Maize Genome Project"

/note="This library represents the unique genes found in the fifth round of EST sequencing at Stanford University for the maize genome project. Sequences are present from library 946. Contigs were assembled using ZMDAssembler and 2 representatives from each contig were selected for the Unigene set. All singlets were also selected."

BASE COUNT 122 a 170 c 160 g 125 t

ORIGIN

Query Match 40.6%; Score 538.2; DB 14; Length 577;

Best Local Similarity 97.6%; Pred. No. 4.2e-46;

Matches 569; Conservative 0; Mismatches 8; Indels 6; Gaps 2;

Qy 74 TACTCCGCTGCATCTCCAAAGCAGCAGTCTCCCTCTGGCTTCCCGCTCTCTCGGCT 133

Db 1 TACTCCGCTGCATCTCCAAAGCAGCAGTCTCCCTCTGGCTTCCCGCTCTCTCGGCT 60

Qy 134 CTTTCGGCTCCGACGCGCCCTCTATGGCCACCGCGCGCGCCGACCGCAGCAGCAGCAG 193

Db 61 CTTTCGGCTCCGACGCGCCCTCTATGGCCACCGCGCGCGCCGACCGCAGCAGCAGCAG 117

Qy 194 TCTCTCCCGCTGCGCGCTGGAGCAGCGCGCGCGCGCGCGCTCCCGCGCGGCTTCG 253

Db 118 TCCTCTCCCGCTGCGCGCTGGAGCAGCGCGCGCGCGCGCTCCCGCGCGGCTTCG 174

Qy 254 TCAGTTTGGTGGAGCGCGCGCTTCTCTCCAGCTGCGGTCCGCGCGGCTTCG 313

Db 175 TCAGTTTGGTGGAGCGCGCGCTTCTCTCCAGCTGCGGTCCGCGCGGCTTCG 234

Qy 314 CTGTTGTGCAACCCATGTTGCTGTTGAACAGCAGTTGTAAGATGCTACCAAGC 373

Db 235 CTGTTGTGCAACCCATGTTGCTGTTGAACAGCAGTTGTAAGATGCTACCAAGC 294

Qy 374 TGGAGCTCCAGTTGTTGTTACAGTGCATCTAGAGGATTTGTAAGCACTGCTC 433

Db 295 TGGAGCTCCAGTTGTTGTTACAGTGCATCTAGAGGATTTGTAAGCACTGCTC 354

Qy 434 TAGCCCTTGAAGAGCAGGATGCAAGGTTCTGGTAAACTATGCCCGTCTCCGAAAGG 493

Db 355 TAGCCCTTGAAGAGCAGGATGCAAGGTTCTGGTAAACTATGCCCGTCTCCGAAAGG 414

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 15:42:35 ; Search time 5006 Seconds
(without alignments)
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- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	50	3.8	3375	6	AR204971 Sequence
2	48	3.6	677	9	AB065088 Homo sapi
3	48	3.6	1210	3	AY069529 Drosophil
4	48	3.6	1522	6	AR153819 Sequence
5	48	3.6	2227	6	AR243792 Sequence
6	48	3.6	2877	9	BC018933 Homo sapi
7	48	3.6	2369	10	BC023786 Mus muscu
8	47	3.5	112	6	AX203306 Sequence
9	47	3.5	575	8	X65154 P.sativum G
10	47	3.5	679	5	AF467914 Danio rer
11	47	3.5	688	6	I03321 Sequence 12
12	47	3.5	899	9	BC053374 Homo sapi
13	47	3.5	902	6	AX478009 Sequence
14	47	3.5	956	9	AL079309 Homo sapi
15	47	3.5	981	9	BC027909 Homo sapi
16	47	3.5	1015	6	BD082470 87 human
17	47	3.5	1100	17	AF111845 Homo sapi
18	47	3.5	1199	9	BC012540 Homo sapi
19	47	3.5	1201	6	AR243066 Sequence
20	47	3.5	1228	9	HSB802894 Homo sapi
21	47	3.5	1265	3	AY119559 Drosophil
22	47	3.5	1275	8	AF297044 Zea mays
23	47	3.5	1358	9	BC013728 Homo sapi
24	47	3.5	1360	9	BC015168 Homo sapi
25	47	3.5	1400	8	AF239828 Petroseli
26	47	3.5	1552	9	BC002411 Homo sapi
27	47	3.5	1705	9	BC043560 Homo sapi
28	47	3.5	1750	9	BC048294 Homo sapi
29	47	3.5	1781	10	BC053434 Mus muscu
30	47	3.5	1911	10	BC048954 Mus muscu
31	47	3.5	2012	9	BC025740 Homo sapi
32	47	3.5	2059	3	AY069067 Drosophil
33	47	3.5	2100	3	BT001318 Drosophil
34	47	3.5	2150	9	BC012148 Homo sapi
35	47	3.5	2210	9	AB066547 Macaca fa
36	47	3.5	2332	9	BC007680 Homo sapi
37	47	3.5	2623	9	BC028978 Homo sapi
38	47	3.5	2651	9	BC013590 Homo sapi
39	47	3.5	2812	10	BC024323 Mus muscu
40	47	3.5	3340	9	BC038451 Homo sapi
41	47	3.5	3468	10	BC027246 Mus muscu
42	47	3.5	3706	3	AY069828 Drosophil
43	47	3.5	3965	9	BC034970 Homo sapi
44	47	3.5	3994	8	TOBEXT N.plumbagin
45	47	3.5	4951	3	AY160092 Dictyoste
46	47	3.5	6548	5	BC047246 Xenopus l
47	47	3.5	64814	2	NCB21J21 Neurospor
48	47	3.5	152841	2	AL929463 Danio rer
49	47	3.5	183583	2	AC101777 Mus muscu
50	47	3.5	208409	2	AC117895 Rattus no
51	47	3.5	240901	2	AC096328 Rattus no
52	47	3.5	246548	2	BX530062 Danio rer
53	47	3.5	254050	3	PFA929358 Plasmodiu
54	46	3.5	130	6	BD116948 EST and e
55	46	3.5	227	9	BC046515 Homo sapi
56	46	3.5	255	3	AF132976 Buthus ma
57	46	3.5	255	6	BD113462 EST and e
58	46	3.5	347	6	A23327 O.sativa mR
59	46	3.5	347	6	I47730 Sequence 2
60	46	3.5	351	6	BD119190 EST and e
61	46	3.5	477	3	AF098065 Trypanoso
62	46	3.5	522	10	MUSXISTAE Li0730 Mouse (clon
63	46	3.5	529	5	BC045069 Xenopus l
64	46	3.5	530	6	AR243058 Sequence
65	46	3.5	532	8	OSAF001396 Oryza sat

C	66	46	3.5	567	6	AX052527	Sequence	139	46	3.5	1411	10	BC039806	BC039806 Mus muscu
	67	46	3.5	580	9	BC042082	BC042082 Homo sapi	140	46	3.5	1420	17	AF119899	AF119899 Homo sapi
	68	46	3.5	585	10	BC021916	BC021916 Mus muscu	141	46	3.5	1433	3	AB080950	AB080950 Ciona int
	69	46	3.5	589	10	BC022135	BC022135 Mus muscu	142	46	3.5	1437	9	BC032310	BC032310 Homo sapi
	70	46	3.5	610	8	AF009959	Oryza sat	143	46	3.5	1451	17	AF118083	AF118083 Homo sapi
	71	46	3.5	615	3	AY075437	AY075437 Drosophi	144	46	3.5	1485	10	BC051057	BC051057 Mus muscu
	72	46	3.5	648	3	AY071113	AY071113 Drosophi	145	46	3.5	1493	9	BC042547	BC042547 Homo sapi
	73	46	3.5	659	3	AY119605	AY119605 Drosophi	146	46	3.5	1493	9	BC043317	BC043317 Homo sapi
	74	46	3.5	680	10	BC038677	BC038677 Mus muscu	147	46	3.5	1498	3	AY069685	AY069685 Drosophi
	75	46	3.5	691	3	HVU48594	U48594 Helicthis v	148	46	3.5	1499	5	BC045520	BC045520 Drosophi
	76	46	3.5	692	5	BC049029	BC049029 Danio rer	149	46	3.5	1499	5	BC045520	BC045520 Danio rer
	77	46	3.5	699	9	AY080839	AY080839 Homo sapi	150	46	3.5	1502	10	BC023687	BC023687 Mus muscu
	78	46	3.5	703	9	AY080839	AY080839 Homo sapi	151	46	3.5	1503	5	BC041249	BC041249 Xenopus l
	79	46	3.5	728	3	AY069234	AY069234 Drosophi	152	46	3.5	1509	9	BC029059	BC029059 Homo sapi
	80	46	3.5	767	9	AK000653	AK000653 Homo sapi	153	46	3.5	1523	9	BC038956	BC038956 Homo sapi
	81	46	3.5	773	6	BD072968	BD072968 70 human	154	46	3.5	1540	9	BC035562	BC035562 Homo sapi
	82	46	3.5	775	9	BC027847	BC027847 Homo sapi	155	46	3.5	1541	9	HSN803748	AL832440 Homo sapi
	83	46	3.5	778	9	BC047942	BC047942 Homo sapi	156	46	3.5	1553	9	BC040262	BC040262 Homo sapi
	84	46	3.5	788	9	BC044829	BC044829 Homo sapi	157	46	3.5	1566	10	BC045149	BC045149 Mus muscu
	85	46	3.5	790	10	BC051504	BC051504 Mus muscu	158	46	3.5	1574	9	BC036048	BC036048 Homo sapi
	86	46	3.5	834	10	BC028766	BC028766 Mus muscu	159	46	3.5	1579	9	BC040355	BC040355 Homo sapi
	87	46	3.5	878	9	BC007499	BC007499 Homo sapi	160	46	3.5	1580	9	AK027109	AK027109 Homo sapi
	88	46	3.5	898	10	BC026633	BC026633 Mus muscu	161	46	3.5	1580	9	BC038840	BC038840 Homo sapi
	89	46	3.5	899	3	AK114040	AK114040 Ciona int	162	46	3.5	1596	8	PSVICK	X67429 Pisum sativ
	90	46	3.5	900	6	SIDERHYDA	Z21500 S. longipes	163	46	3.5	1615	9	AB050410	AB050410 Macaca fa
	91	46	3.5	901	6	AX305939	AX305939 Sequence	164	46	3.5	1617	10	BC024572	BC024572 Mus muscu
	92	46	3.5	901	10	MUSNASCHY2	M68899 Mouse mast	165	46	3.5	1620	3	AY069829	AY069829 Drosophi
	93	46	3.5	923	3	AY070496	AY070496 Drosophi	166	46	3.5	1620	10	BC003888	BC003888 Mus muscu
	94	46	3.5	929	3	AY118282	AY118282 Drosophi	167	46	3.5	1626	9	AB060876	AB060876 Macaca fa
	95	46	3.5	930	3	AY075318	AY075318 Drosophi	168	46	3.5	1630	9	BC048341	BC048341 Homo sapi
	96	46	3.5	979	9	BC023583	BC023583 Homo sapi	169	46	3.5	1637	3	AK112340	AK112340 Ciona int
	97	46	3.5	985	9	BC051265	BC051265 Homo sapi	170	46	3.5	1637	6	AX460089	AX460089 Sequence
	98	46	3.5	1010	9	BC035795	BC035795 Homo sapi	171	46	3.5	1640	10	BC052156	BC052156 Mus muscu
	99	46	3.5	1020	3	AY118958	AY118958 Drosophi	172	46	3.5	1645	10	BC046317	BC046317 Mus muscu
	100	46	3.5	1020	8	AF236374	AF236374 Zea mays	173	46	3.5	1647	8	AF124842	AF124842 Capsicum
	101	46	3.5	1024	9	BC013602	BC013602 Homo sapi	174	46	3.5	1650	9	BC009332	BC009332 Homo sapi
	102	46	3.5	1027	9	BC035292	BC035292 Homo sapi	175	46	3.5	1653	10	BC018365	BC018365 Mus muscu
	103	46	3.5	1056	10	BC034844	BC034844 Mus muscu	176	46	3.5	1655	10	BC051403	BC051403 Mus muscu
	104	46	3.5	1057	5	BC047199	BC047199 Danio rer	177	46	3.5	1658	10	BC031470	BC031470 Mus muscu
	105	46	3.5	1065	6	AX644278	AX644278 Sequence	178	46	3.5	1660	6	AR243159	AR243159 Sequence
	106	46	3.5	1079	10	BC051970	BC051970 Mus muscu	179	46	3.5	1660	10	BC052328	BC052328 Mus muscu
	107	46	3.5	1084	9	BC009977	BC009977 Homo sapi	180	46	3.5	1662	9	BC011515	BC011515 Homo sapi
	108	46	3.5	1090	9	BC047013	BC047013 Homo sapi	181	46	3.5	1665	5	AF080068	AF080068 Xenopus l
	109	46	3.5	1097	10	BC008270	BC008270 Mus muscu	182	46	3.5	1686	9	BC025279	BC025279 Homo sapi
	110	46	3.5	1114	3	AY118558	AY118558 Drosophi	183	46	3.5	1688	9	AK025117	AK025117 Homo sapi
	111	46	3.5	1121	9	BC003658	BC003658 Homo sapi	184	46	3.5	1688	9	BC004839	BC004839 Homo sapi
	112	46	3.5	1126	10	BC022681	BC022681 Mus muscu	185	46	3.5	1690	9	BC037960	BC037960 Homo sapi
	113	46	3.5	1130	9	BC007659	BC007659 Homo sapi	186	46	3.5	1710	9	BC033591	BC033591 Homo sapi
	114	46	3.5	1144	10	BC028796	BC028796 Mus muscu	187	46	3.5	1736	9	BC016023	BC016023 Homo sapi
	115	46	3.5	1162	9	BC017328	BC017328 Homo sapi	188	46	3.5	1738	9	BC014399	BC014399 Homo sapi
	116	46	3.5	1168	9	BC042156	BC042156 Homo sapi	189	46	3.5	1743	10	BC051150	BC051150 Mus muscu
	117	46	3.5	1170	9	BC040374	BC040374 Homo sapi	190	46	3.5	1744	3	AY069796	AY069796 Drosophi
	118	46	3.5	1179	10	BC003972	BC003972 Mus muscu	191	46	3.5	1756	6	BD006863	BD006863 Drosophi
	119	46	3.5	1188	9	BC017237	BC017237 Homo sapi	192	46	3.5	1756	9	AF143723	AF143723 Homo sapi
	120	46	3.5	1200	10	BC030371	BC030371 Mus muscu	193	46	3.5	1758	9	BC018214	BC018214 Homo sapi
	121	46	3.5	1204	8	CR275305	AJ275305 Cicer ari	194	46	3.5	1760	9	BC033862	BC033862 Homo sapi
	122	46	3.5	1207	9	BC024650	BC024650 Homo sapi	195	46	3.5	1761	9	BC006103	BC006103 Homo sapi
	123	46	3.5	1240	9	AK026633	AK026633 Homo sapi	196	46	3.5	1773	9	BC035667	BC035667 Homo sapi
	124	46	3.5	1240	10	BC030163	BC030163 Mus muscu	197	46	3.5	1776	9	HSN804574	HSN804574 Homo sapi
	125	46	3.5	1243	9	BC047691	BC047691 Homo sapi	198	46	3.5	1779	10	BC016197	BC016197 Mus muscu
	126	46	3.5	1257	9	AK027099	AK027099 Homo sapi	199	46	3.5	1780	9	BC020590	BC020590 Homo sapi
	127	46	3.5	1265	9	BC033301	BC033301 Homo sapi	200	46	3.5	1794	3	AB031232	AB031232 Toxoplas
	128	46	3.5	1273	9	BC020566	BC020566 Homo sapi	201	46	3.5	1796	9	AB070144	AB070144 Macaca fa
	129	46	3.5	1279	8	LSB297917	AJ297917 Lycopersi	202	46	3.5	1796	10	BC026588	BC026588 Mus muscu
	130	46	3.5	1307	10	BC038008	BC038008 Mus muscu	203	46	3.5	1798	8	AF521906	AF521906 Hebeloma
	131	46	3.5	1309	5	BC052141	BC052141 Danio rer	204	46	3.5	1802	9	AB047947	AB047947 Macaca fa
	132	46	3.5	1330	9	BC037584	BC037584 Homo sapi	205	46	3.5	1814	9	BC044249	BC044249 Homo sapi
	133	46	3.5	1331	9	AK024588	AK024588 Homo sapi	206	46	3.5	1816	9	BC041173	BC041173 Homo sapi
	134	46	3.5	1357	10	BC026868	BC026868 Mus muscu	207	46	3.5	1820	6	BD130976	BD130976 Homo sapi
	135	46	3.5	1366	10	BC024950	BC024950 Mus muscu	208	46	3.5	1832	9	BC025310	BC025310 Homo sapi
	136	46	3.5	1368	10	BC020029	BC020029 Mus muscu	209	46	3.5	1841	9	AB072773	AB072773 Macaca fa
	137	46	3.5	1371	3	AY089518	AY089518 Drosophi	210	46	3.5	1844	6	E16086	E16086 cDNA encodi
	138	46	3.5	1394	9	AK000418	AK000418 Homo sapi	211	46	3.5	1872	6	AR205050	AR205050 Sequence

212	46	3.5	1872	6	AX615066 Sequence	285	46	3.5	2530	9	BC037544	BC037544 Homo sapi
213	46	3.5	1878	9	HSMB03563	286	46	3.5	2532	9	HSMB05209	AL833903 Homo sapi
214	46	3.5	1889	9	BC050462 Homo sapi	287	46	3.5	2538	9	BC014055	BC014055 Homo sapi
215	46	3.5	1900	3	AY113313 Drosophila	288	46	3.5	2540	9	BC053655	BC053655 Homo sapi
216	46	3.5	1902	9	AB047930 Macaca fa	289	46	3.5	2540	10	AB047324	AB047324 Rattus no
217	46	3.5	1902	9	BC048252 Homo sapi	290	46	3.5	2544	9	BC012343	BC012343 Homo sapi
218	46	3.5	1910	10	BC003738 Mus muscu	291	46	3.5	2560	9	AK027260	AK027260 Homo sapi
219	46	3.5	1913	9	BC017207 Homo sapi	292	46	3.5	2560	9	AB059653	AB059653 Macaca fa
220	46	3.5	1914	10	BC013523 Mus muscu	293	46	3.5	2604	9	HSMB05664	AL834537 Homo sapi
221	46	3.5	1927	5	BC045519 Danio rer	294	46	3.5	2605	9	BC036855	BC036855 Homo sapi
222	46	3.5	1935	10	BC026141 Mus muscu	295	46	3.5	2611	9	AK027152	AK027152 Homo sapi
223	46	3.5	1934	9	BC036327 Homo sapi	296	46	3.5	2619	9	AF068229	AF068229 Homo sapi
224	46	3.5	1965	3	AY069659 Drosophila	297	46	3.5	2625	6	AF164818	AF164818 Sequence
225	46	3.5	1968	10	BC027123 Mus muscu	298	46	3.5	2642	10	AS086166	AB086166 Mus muscu
226	46	3.5	1978	9	AK026762 Homo sapi	299	46	3.5	2666	3	AY069037	AY069037 Drosophila
227	46	3.5	1987	9	BC012750 Homo sapi	300	46	3.5	2674	5	BC051620	BC051620 Danio rer
228	46	3.5	1999	4	BTU52688 Bos taurus	301	46	3.5	2676	10	BC031754	BC031754 Mus muscu
229	46	3.5	2001	5	BC051623 Homo sapi	302	46	3.5	2690	10	BC051054	BC051054 Mus muscu
230	46	3.5	2026	9	BC022399 Homo sapi	303	46	3.5	2705	10	BC021341	BC021341 Mus muscu
231	46	3.5	2033	3	AK116646 Ciona int	304	46	3.5	2729	9	HSMB02938	X78627 H. sapiens m
232	46	3.5	2038	9	BC016758 Homo sapi	305	46	3.5	2758	9	HSMB02938	AL583915 Homo sapi
233	46	3.5	2038	9	BC043591 Homo sapi	306	46	3.5	2762	8	AFS30051	AFS30051 Chlamydom
234	46	3.5	2038	10	BC025004 Mus muscu	307	46	3.5	2783	9	BC027877	BC027877 Homo sapi
235	46	3.5	2043	10	BC052188 Mus muscu	308	46	3.5	2785	9	HSMB04684	BC047540 Homo sapi
236	46	3.5	2045	9	IR2004595 Homo sapi	309	46	3.5	2807	9	BC047540	BC047540 Homo sapi
237	46	3.5	2059	9	BC025708 Homo sapi	310	46	3.5	2815	9	BC014834	BC014834 Homo sapi
238	46	3.5	2068	9	AF103804 Homo sapi	311	46	3.5	2825	3	AY070545	AY070545 Drosophila
239	46	3.5	2080	9	BC008717 Homo sapi	312	46	3.5	2826	9	BC040919	BC040919 Homo sapi
240	46	3.5	2081	10	BC043712 Mus muscu	313	46	3.5	2832	9	HSMB03459	AL832152 Homo sapi
241	46	3.5	2096	9	BC033808 Homo sapi	314	46	3.5	2837	6	AR083283	AR083283 Sequence
242	46	3.5	2105	9	BC017272 Homo sapi	315	46	3.5	2837	6	AD099547	AD099547 Sequence
243	46	3.5	2105	10	BC047133 Mus muscu	316	46	3.5	2837	6	AD099547	BD056699 Secreted
244	46	3.5	2111	9	HSMB05194 Homo sapi	317	46	3.5	2897	6	AR088747	AR088747 Sequence
245	46	3.5	2112	6	AX535011 Sequence	318	46	3.5	2897	6	AR270600	AR270600 Sequence
246	46	3.5	2116	9	BC034379 Homo sapi	319	46	3.5	2897	9	HSU66075	U66075 Human trans
247	46	3.5	2128	10	BC049994 Mus muscu	320	46	3.5	2905	10	AY029302	AY029302 Rattus no
248	46	3.5	2130	3	AK112217 Ciona int	321	46	3.5	2955	10	BC025427	BC025427 Mus muscu
249	46	3.5	2130	9	BC032389 Homo sapi	322	46	3.5	2964	9	BC018366	BC018366 Homo sapi
250	46	3.5	2136	6	AR252575 Sequence	323	46	3.5	2967	9	BC044952	BC044952 Homo sapi
251	46	3.5	2136	6	AX376160 Sequence	324	46	3.5	2997	10	BC026819	BC026819 Mus muscu
252	46	3.5	2136	6	AX043415 Sequence	325	46	3.5	2997	10	MMPTAI13A	X69026 M. musculus
253	46	3.5	2139	9	AY089322 Drosophila	326	46	3.5	3003	6	AX086957	AX086957 Sequence
254	46	3.5	2153	9	AB049880 Macaca fa	327	46	3.5	3003	9	HSMB01863	AL136895 Homo sapi
255	46	3.5	2159	9	HSMB00763 Homo sapi	328	46	3.5	3006	6	AX497163	AX497163 Sequence
256	46	3.5	2177	9	BC043383 Homo sapi	329	46	3.5	3007	9	BC036067	BC036067 Homo sapi
257	46	3.5	2178	9	BC034740 Homo sapi	330	46	3.5	3040	9	BC036235	BC036235 Homo sapi
258	46	3.5	2209	9	BC034762 Homo sapi	331	46	3.5	3059	10	BC051082	BC051082 Mus muscu
259	46	3.5	2235	6	AR275257 Sequence	332	46	3.5	3077	10	BC026138	BC026138 Mus muscu
260	46	3.5	2235	6	AX049445 Sequence	333	46	3.5	3082	10	BC046972	BC046972 Mus muscu
261	46	3.5	2246	10	AF026124 Mus muscu	334	46	3.5	3122	9	BC030654	BC030654 Homo sapi
262	46	3.5	2256	3	AY069791 Drosophila	335	46	3.5	3122	9	BC041133	BC041133 Homo sapi
263	46	3.5	2267	6	E01314 cDNA encodi	336	46	3.5	3169	5	AB031070	AB031070 Cyprinus
264	46	3.5	2283	9	AK000257 Homo sapi	337	46	3.5	3244	3	BT003295	BT003295 Homo sapi
265	46	3.5	2289	3	AK114795 Ciona int	338	46	3.5	3276	3	BT003295	BT003295 Drosophila
266	46	3.5	2296	9	HSMB02712 Homo sapi	339	46	3.5	3307	10	BC018613	BC018613 Mus muscu
267	46	3.5	2298	10	BC049257 Mus muscu	340	46	3.5	3347	8	AT011828	AT011828 Arabidops
268	46	3.5	2322	9	BC028041 Homo sapi	341	46	3.5	3348	8	AT011828	AX011628 Arabidops
269	46	3.5	2325	10	RNU30290 Rattus norv	342	46	3.5	3376	6	AX284970	AX284970 Sequence
270	46	3.5	2328	9	BC007567 Homo sapi	343	46	3.5	3386	9	HSMB00161	AL050092 Homo sapi
271	46	3.5	2345	9	AK027144 Homo sapi	344	46	3.5	3506	9	HSMB03163	AL831846 Homo sapi
272	46	3.5	2360	10	BC008547 Mus muscu	345	46	3.5	3513	6	AX277590	AX277590 Sequence
273	46	3.5	2389	9	BC014941 Homo sapi	346	46	3.5	3513	9	HSMB00944	AL117435 Homo sapi
274	46	3.5	2409	9	BC034925 Homo sapi	347	46	3.5	3521	6	AX382070	AX382070 Sequence
275	46	3.5	2437	9	BC018610 Homo sapi	348	46	3.5	3575	9	HSMB02410	AL137641 Homo sapi
276	46	3.5	2438	9	BC001056 Homo sapi	349	46	3.5	3587	10	BC016669	BC016669 Mus muscu
277	46	3.5	2438	9	BC001056 Homo sapi	350	46	3.5	3606	9	BC015897	BC015897 Homo sapi
278	46	3.5	2440	8	AS021862 Cucumis m	351	46	3.5	3619	9	HSMB05213	AL833907 Homo sapi
279	46	3.5	2445	9	BC048285 Homo sapi	352	46	3.5	3655	9	BC013382	BC013382 Homo sapi
280	46	3.5	2446	9	BC032448 Homo sapi	353	46	3.5	3710	9	BC035723	BC035723 Homo sapi
281	46	3.5	2462	9	HSMB000419 Homo sapi	354	46	3.5	3715	6	AR277694	AR277694 Sequence
282	46	3.5	2494	9	AF262032 Homo sapi	355	46	3.5	3715	10	MMU35846	U35846 Mus muscu
283	46	3.5	2514	9	BC049384 Homo sapi	356	46	3.5	3744	9	BC038299	BC038299 Homo sapi
284	46	3.5	2523	9	BC037218 Homo sapi	357	46	3.5	3838	9	BC026226	BC026226 Homo sapi

358	46	3.5	3860	9	BC035683	BC035683 Homo sapi	C 431	46	3.5	172132	9	AC010149	AC010149 Homo sapi
359	46	3.5	4010	9	BC035599	BC035599 Homo sapi	432	46	3.5	172665	10	AL645740	AL645740 Mouse DNA
360	46	3.5	4036	10	MMU278263	AJ278263 Mus muscu	433	46	3.5	176149	2	EX294129	EX294129 Danio rer
361	46	3.5	4080	10	BC051641	BC051641 Mus muscu	C 434	46	3.5	176149	2	EX294129	EX294129 Danio rer
362	46	3.5	4142	9	HSM800682	AL080163 Homo sapi	435	46	3.5	176440	9	AC104675	AC104675 Sus scrofa
363	46	3.5	4152	10	BC043657	BC043657 Mus muscu	436	46	3.5	176601	9	AC073581	AC073581 Homo sapi
364	46	3.5	4212	9	HSM800772	AL110269 Homo sapi	437	46	3.5	177020	2	AC141484	AC141484 Mus muscu
365	46	3.5	4250	9	BC036749	BC036749 Homo sapi	438	46	3.5	177149	2	AC141484	AC141484 Mus muscu
366	46	3.5	4297	9	BC018928	BC018928 Homo sapi	439	46	3.5	178517	10	AC121905	AC121905 Mus muscu
367	46	3.5	4505	9	HSM803050	AL713378 Homo sapi	C 440	46	3.5	178981	10	AL806511	AL806511 Mouse DNA
368	46	3.5	4620	9	BC033494	BC033494 Homo sapi	C 441	46	3.5	179548	2	AC131596	AC131596 Mus muscu
369	46	3.5	4656	9	HSM803142	AL831828 Homo sapi	442	46	3.5	180849	2	EX465857	EX465857 Danio rer
370	46	3.5	4730	9	BC036755	AL831828 Homo sapi	443	46	3.5	181534	2	AC113065	AC113065 Mus muscu
371	46	3.5	4869	3	AY113238	BC036755 Homo sapi	C 444	46	3.5	183412	2	AP001899	AP001899 Homo sapi
372	46	3.5	5120	6	AX710220	AX710220 Sequence	445	46	3.5	184121	9	AC016706	AC016706 Homo sapi
373	46	3.5	5130	9	HSM801717	AL136749 Homo sapi	C 446	46	3.5	186574	2	AC123827	AC123827 Mus muscu
374	46	3.5	5440	6	AX710219	AX710219 Sequence	C 447	46	3.5	187904	2	AC119843	AC119843 Mus muscu
375	46	3.5	5465	3	AY051653	AY051653 Drosophila	C 448	46	3.5	190517	9	CNS01DX4	AL139022 Human chr
376	46	3.5	5856	9	HSM803500	AL831933 Homo sapi	C 449	46	3.5	191733	10	AC121774	AC121774 Mus muscu
377	46	3.5	6153	6	BD160662	BD160662 Primer fo	C 450	46	3.5	193108	10	AL671977	AL671977 Mouse DNA
378	46	3.5	6153	9	AK027868	AK027868 Homo sapi	C 451	46	3.5	193108	10	AL671977	AL671977 Mouse DNA
379	46	3.5	6251	10	BC050823	BC050823 Mus muscu	452	46	3.5	194124	2	EX294189	EX294189 Danio rer
380	46	3.5	6410	9	AF230496	AF230496 Homo sapi	453	46	3.5	196421	10	AL672100	AL672100 Mouse DNA
C 381	46	3.5	6660	10	AF447902	AF447902 Mus muscu	C 454	46	3.5	196421	10	AL672100	AL672100 Mouse DNA
382	46	3.5	6791	6	AG0092	AG0092 Sequence 2	C 455	46	3.5	198185	2	AC131323	AC131323 Mus muscu
383	46	3.5	10195	6	AG0094	AG0094 Sequence 4	C 456	46	3.5	198185	2	AC131323	AC131323 Mus muscu
384	46	3.5	10919	10	AF031572	AF031572 Mus muscu	C 457	46	3.5	198185	2	AC131323	AC131323 Mus muscu
385	46	3.5	12029	3	AE001400	AE001400 Plasmodiu	C 458	46	3.5	199394	10	AL723370	AL723370 Mouse DNA
C 386	46	3.5	12463	3	AC115578	AC115578 Dictyoste	C 459	46	3.5	200059	9	AL355136	AL355136 Human DNA
387	46	3.5	33651	3	AC114261	AC114261 Dictyoste	C 460	46	3.5	200075	2	AC127302	AC127302 Mus muscu
C 388	46	3.5	37599	9	AP000532	AP000532 Homo sapi	C 461	46	3.5	200616	2	AC132240	AC132240 Mus muscu
389	46	3.5	38692	3	AC116919	AC116919 Dictyoste	C 462	46	3.5	203422	10	AL713863	AL713863 Mouse DNA
390	46	3.5	40992	9	AC002471	AC002471 Homo sapi	C 463	46	3.5	203422	10	AL713863	AL713863 Mouse DNA
391	46	3.5	41958	5	AL591170	AL591170 Homo sapi	C 464	46	3.5	204166	2	AC121451	AC121451 Rattus no
C 392	46	3.5	80272	5	AL591180	AL591180 Zebrafish	C 465	46	3.5	204166	2	AC121451	AC121451 Rattus no
C 393	46	3.5	82848	5	AL645689	AL645689 Zebrafish	C 466	46	3.5	207823	2	AC114425	AC114425 Mus muscu
C 394	46	3.5	89232	5	AL591175	AL591175 Zebrafish	C 467	46	3.5	210005	2	AC118299	AC118299 Rattus no
C 395	46	3.5	92496	9	AL589848	AL589848 Human DNA	C 468	46	3.5	210005	2	AC118299	AC118299 Rattus no
C 396	46	3.5	109143	10	AL845448	AL845448 Mouse DNA	C 469	46	3.5	212410	2	AC118804	AC118804 Rattus no
C 397	46	3.5	110000	2	AC102983	Continuation (2 of	C 470	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 398	46	3.5	110000	2	AC111440	Continuation (2 of	C 471	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 399	46	3.5	110000	2	EX005003	Continuation (3 of	C 472	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 400	46	3.5	110000	2	EX284615	EX284615 Mus muscu	C 473	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 401	46	3.5	110000	2	EX238632	Continuation (3 of	C 474	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 402	46	3.5	110000	3	AC116305	Continuation (4 of	C 475	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 403	46	3.5	110000	3	AC116984	AC116984 Dictyoste	C 476	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 404	46	3.5	110000	3	AC116984	Continuation (4 of	C 477	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 405	46	3.5	123701	9	AC010137	AC010137 Homo sapi	C 478	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 406	46	3.5	135774	2	AC091380	AC091380 Mus muscu	C 479	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 407	46	3.5	136956	2	AC137338	AC137338 Rattus no	C 480	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 408	46	3.5	137648	2	AC024316	AC024316 Homo sapi	C 481	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 409	46	3.5	141009	2	AC009425	AC009425 Homo sapi	C 482	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 410	46	3.5	142100	2	EX511181	EX511181 Danio rer	C 483	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 411	46	3.5	145700	3	AC117072	AC117072 Dictyoste	C 484	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 412	46	3.5	147952	9	AC008712	AC008712 Homo sapi	C 485	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 413	46	3.5	148295	2	AL662913	AL662913 Homo sapi	C 486	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 414	46	3.5	150509	2	AC113453	AC113453 Mus muscu	C 487	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 415	46	3.5	152829	2	AC132267	AC132267 Mus muscu	C 488	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 416	46	3.5	153139	2	AC129296	AC129296 Mus muscu	C 489	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 417	46	3.5	153228	2	AC139129	AC139129 Mus muscu	C 490	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 418	46	3.5	153228	2	AC139129	AC139129 Mus muscu	C 491	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 419	46	3.5	156446	2	AC144774	AC144774 Mus muscu	C 492	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 420	46	3.5	157667	2	AC115970	AC115970 Mus muscu	C 493	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 421	46	3.5	161674	10	AL807394	AL807394 Mouse DNA	C 494	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 422	46	3.5	161931	2	AC117903	AC117903 Rattus no	C 495	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 423	46	3.5	163829	2	AC136048	AC136048 Rattus no	C 496	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 424	46	3.5	165104	2	EX511213	EX511213 Danio rer	C 497	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 425	46	3.5	167357	2	AC023873	AC023873 Homo sapi	C 498	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 426	46	3.5	167409	10	AC121982	AC121982 Mus muscu	C 499	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 427	46	3.5	168544	9	AL133344	AL133344 Human DNA	C 500	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 428	46	3.5	169825	2	AC102577	AC102577 Mus muscu	C 501	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 429	46	3.5	170053	2	AC133069	AC133069 Macaca mu	C 502	46	3.5	212604	2	AC095966	AC095966 Rattus no
C 430	46	3.5	171076	2	AC101857	AC101857 Mus muscu	C 503	46	3.5	212604	2	AC095966	AC095966 Rattus no

504	46	3.5	332036	2	AC129629	AC129629 Rattus no	577	45	3.4	958	6	AR217518	AR217518 Sequence
c 505	46	3.5	343753	2	AC129332	AC129332 Mus muscu	578	45	3.4	958	6	AR233975	AR233975 Sequence
c 506	46	3.5	346007	2	AC114921	AC114921 Mus muscu	579	45	3.4	958	6	AX250563	AX250563 Sequence
507	45	3.4	91	91	BD118981	BD118981 EST and e	580	45	3.4	958	6	BD056504	BD056504 Apparatus
508	45	3.4	184	6	BD116949	BD116949 EST and e	581	45	3.4	958	6	BD137222	BD137222 Luciferase
509	45	3.4	188	6	AX341368	AX341368 Sequence	582	45	3.4	958	6	E01573	E01573 cDNA sequen
c 510	45	3.4	293	6	AX187087	AX187087 Sequence	583	45	3.4	958	6	E01575	E01575 cDNA sequen
c 511	45	3.4	308	6	AX329898	AX329898 Sequence	584	45	3.4	958	6	E02319	E02319 DNA encodin
c 512	45	3.4	308	6	AX330637	AX330637 Sequence	585	45	3.4	958	6	HSM800632	HSM800632 Homo sapi
c 513	45	3.4	308	6	AX330821	AX330821 Sequence	586	45	3.4	985	9	HS4420492	HS4420492 Homo sapi
c 514	45	3.4	332	6	AX185622	AX185622 Sequence	587	45	3.4	992	9	HSRANAP1	HSRANAP1 Homo sapi
c 515	45	3.4	358	6	BD108843	BD108843 EST and e	588	45	3.4	1026	8	AF179295	AF179295 Malus dom
516	45	3.4	372	9	BD015361	BD015361 Homo sapi	589	45	3.4	1026	8	AK027111	AK027111 Homo sapi
517	45	3.4	380	9	HSWUC5BR	Y10080 H.sapiens M	590	45	3.4	1028	10	BC002172	BC002172 Mus muscu
518	45	3.4	447	9	AC026855	AC026855 Homo sapi	591	45	3.4	1030	9	BC000895	BC000895 Homo sapi
519	45	3.4	473	9	BC051840	BC051840 Homo sapi	592	45	3.4	1032	8	AF043538	AF043538 Arabidops
520	45	3.4	476	8	AY157064	AY157064 Lycopersi	593	45	3.4	1035	3	CIN431687	AY431687 Ciona int
521	45	3.4	488	9	BC003678	BC003678 Homo sapi	594	45	3.4	1040	9	BC036737	BC036737 Homo sapi
522	45	3.4	512	3	AK115330	AK115330 Ciona int	595	45	3.4	1042	9	BC021232	BC021232 Homo sapi
523	45	3.4	518	8	QSAJ692	BC000692 Quercus s	596	45	3.4	1045	3	AY075210	AY075210 Drosophil
524	45	3.4	561	10	BC049674	BC049674 Mus muscu	597	45	3.4	1045	9	BC022357	BC022357 Homo sapi
525	45	3.4	570	3	AK112184	AK112184 Ciona int	598	45	3.4	1058	10	BC052508	BC052508 Mus muscu
526	45	3.4	574	9	AK025408	AK025408 Homo sapi	599	45	3.4	1075	6	AR150950	AR150950 Sequence
527	45	3.4	595	6	AX090442	AX090442 Sequence	600	45	3.4	1078	10	AF391160	AF391160 Mus muscu
528	45	3.4	602	9	BC008488	BC008488 Homo sapi	601	45	3.4	1081	3	AY069038	AY069038 Drosophil
529	45	3.4	631	10	BC049570	BC049570 Mus muscu	602	45	3.4	1088	3	BT003646	BT003646 Drosophil
530	45	3.4	691	6	AX011676	AX011676 Sequence	603	45	3.4	1091	6	AR271010	AR271010 Sequence
531	45	3.4	705	8	AF180373	AF180373 Medicago	604	45	3.4	1091	6	AX053122	AX053122 Sequence
532	45	3.4	726	3	AY094790	AY094790 Drosophil	605	45	3.4	1107	9	BC014072	BC014072 Homo sapi
533	45	3.4	740	6	AY066486	AY066486 Sequence	606	45	3.4	1110	9	BC033649	BC033649 Homo sapi
534	45	3.4	740	6	AR074039	AR074039 Sequence	607	45	3.4	1112	9	BC009201	BC009201 Homo sapi
535	45	3.4	740	6	AR143611	AR143611 Sequence	608	45	3.4	1116	9	BC039532	BC039532 Homo sapi
536	45	3.4	740	6	AR216334	AR216334 Sequence	609	45	3.4	1120	9	BC043577	BC043577 Homo sapi
537	45	3.4	740	6	BD005647	BD005647 Materials	610	45	3.4	1126	5	AB090368	AB090368 Takifugu
538	45	3.4	741	6	AR074149	AR074149 Sequence	611	45	3.4	1127	3	AK115583	AK115583 Ciona int
539	45	3.4	741	6	AR216384	AR216384 Sequence	612	45	3.4	1129	9	BC013587	BC013587 Homo sapi
540	45	3.4	741	6	BD005697	BD005697 Materials	613	45	3.4	1139	9	BC030517	BC030517 Homo sapi
541	45	3.4	745	9	BC047941	BC047941 Homo sapi	614	45	3.4	1141	10	BC023104	BC023104 Mus muscu
542	45	3.4	751	9	AF412816	AF412816 Homo sapi	615	45	3.4	1145	10	BC024912	BC024912 Mus muscu
543	45	3.4	752	9	AF475095	AF475095 Homo sapi	616	45	3.4	1152	9	BC021621	BC021621 Homo sapi
544	45	3.4	756	6	AX040689	AX040689 Sequence	617	45	3.4	1157	9	BC013427	BC013427 Homo sapi
545	45	3.4	764	9	BC047904	BC047904 Macaca fa	618	45	3.4	1159	17	AF119883	AF119883 Homo sapi
546	45	3.4	768	10	BC019779	BC019779 Mus muscu	619	45	3.4	1161	9	BC015991	BC015991 Homo sapi
547	45	3.4	781	10	BC028530	BC028530 Mus muscu	620	45	3.4	1182	10	BC003890	BC003890 Mus muscu
548	45	3.4	783	8	CCFCP10	AJ000972 Cyclolell	621	45	3.4	1189	9	AK026104	AK026104 Homo sapi
549	45	3.4	783	9	BC017733	BC017733 Homo sapi	622	45	3.4	1203	10	BC031854	BC031854 Mus muscu
550	45	3.4	788	6	AR216422	AR216422 Sequence	623	45	3.4	1212	6	AR210335	AR210335 Sequence
551	45	3.4	822	10	BC028504	BC028504 Mus muscu	624	45	3.4	1212	6	AR210336	AR210336 Sequence
552	45	3.4	826	6	E08516	E08516 DNA encodin	625	45	3.4	1212	9	AF100781	AF100781 Homo sapi
553	45	3.4	826	6	E12586	E12586 cDNA encodi	626	45	3.4	1228	9	BC002577	BC002577 Homo sapi
554	45	3.4	826	8	S65048	S65048 self-incomp	627	45	3.4	1229	10	BC030860	BC030860 Mus muscu
555	45	3.4	834	10	AF115410	AF115410 Cricetulu	628	45	3.4	1230	5	BC046022	BC046022 Danio rer
556	45	3.4	835	8	ATP27A	Y11792 A.thaliana	629	45	3.4	1243	9	BC034709	BC034709 Homo sapi
557	45	3.4	840	10	BC026668	BC026668 Mus muscu	630	45	3.4	1243	9	HSM802621	HSM802621 Homo sapi
558	45	3.4	844	6	AX105299	AX105299 Sequence	631	45	3.4	1256	17	AF119894	AF119894 Homo sapi
559	45	3.4	848	5	BC044005	BC044005 Xenopus l	632	45	3.4	1263	6	AX546767	AX546767 Sequence
560	45	3.4	848	10	BC018351	BC018351 Mus muscu	633	45	3.4	1271	10	AF161699	AF161699 Mus muscu
561	45	3.4	861	9	AK026600	AK026600 Homo sapi	634	45	3.4	1286	10	BC019521	BC019521 Mus muscu
562	45	3.4	874	10	BC043922	BC043922 Mus muscu	635	45	3.4	1289	10	BC026842	BC026842 Mus muscu
563	45	3.4	887	9	BC015166	BC015166 Homo sapi	636	45	3.4	1296	9	BC009221	BC009221 Homo sapi
564	45	3.4	920	9	BC041137	BC041137 Homo sapi	637	45	3.4	1299	10	BC021404	BC021404 Mus muscu
565	45	3.4	921	10	BC006040	BC006040 Mus muscu	638	45	3.4	1303	10	BC004060	BC004060 Mus muscu
566	45	3.4	925	3	BEVQA440X	L29571 Aequorea vi	639	45	3.4	1307	6	AX578117	AX578117 Sequence
567	45	3.4	932	9	BC047912	BC047912 Homo sapi	640	45	3.4	1313	9	AB048994	AB048994 Macaca fa
568	45	3.4	938	6	A70386	A70386 Sequence 16	641	45	3.4	1315	6	AR173812	AR173812 Sequence
569	45	3.4	938	6	BD010516	BD010516 A novel h	642	45	3.4	1315	10	AF082526	AF082526 Mus muscu
570	45	3.4	941	6	AI15345	AI15345 Bam Hi huma	643	45	3.4	1317	10	BC038528	BC038528 Mus muscu
571	45	3.4	941	6	I03096	I03096 Sequence 8	644	45	3.4	1331	10	BC030915	BC030915 Mus muscu
572	45	3.4	953	3	TVCP4	X77221 T.vaginalis	645	45	3.4	1340	6	AX704811	AX704811 Sequence
573	45	3.4	958	6	AR108851	AR108851 Sequence	646	45	3.4	1346	9	BC042079	BC042079 Homo sapi
574	45	3.4	958	6	AR119320	AR119320 Sequence	647	45	3.4	1347	9	AK026504	AK026504 Homo sapi
575	45	3.4	958	6	AR151721	AR151721 Sequence	648	45	3.4	1351	9	BC004261	BC004261 Homo sapi
576	45	3.4	958	6	AR151721	AR151721 Sequence	649	45	3.4	1360	10	BC046762	BC046762 Mus muscu

650	45	3.4	1372	9	HSB800085	Al0493300 Homo sapi	723	45	3.4	1797	6	AX236928	Sequence
651	45	3.4	1373	10	BC049731	BC049731 Mus muscu	724	45	3.4	1799	9	BC030249	Homo sapi
652	45	3.4	1389	9	BC006210	BC006210 Homo sapi	725	45	3.4	1807	9	BC029917	Homo sapi
653	45	3.4	1400	10	BC037690	BC037690 Mus muscu	726	45	3.4	1817	9	BC051809	Homo sapi
654	45	3.4	1406	9	BC011912	BC011912 Homo sapi	727	45	3.4	1822	3	AY051627	Drosophila
655	45	3.4	1417	9	BC043372	BC043372 Homo sapi	728	45	3.4	1825	9	BC015110	Homo sapi
656	45	3.4	1427	9	BC028022	BC028022 Homo sapi	729	45	3.4	1827	5	BC049315	Danio rer
657	45	3.4	1431	3	AK116801	AK116801 Clona int	730	45	3.4	1827	9	BC034435	Homo sapi
658	45	3.4	1435	10	BC015086	BC015086 Mus muscu	731	45	3.4	1830	9	BC035749	Homo sapi
659	45	3.4	1443	10	BC018470	BC018470 Mus muscu	732	45	3.4	1833	9	BC041158	Homo sapi
660	45	3.4	1445	9	HSB802527	AL1162008 Homo sapi	733	45	3.4	1835	6	AR202048	Sequence
661	45	3.4	1448	9	BC038355	BC038355 Homo sapi	734	45	3.4	1837	10	S69385	epithelial
662	45	3.4	1449	9	BC011460	BC011460 Homo sapi	735	45	3.4	1853	9	HSU58996	US9896 Homo sapien
663	45	3.4	1459	3	AK113466	AK113466 Clona int	736	45	3.4	1857	3	AY113330	Drosophila
664	45	3.4	1463	10	BC005424	BC005424 Mus muscu	737	45	3.4	1860	5	BC046076	Danio rer
665	45	3.4	1464	10	BC002075	BC002075 Mus muscu	738	45	3.4	1868	9	AK026549	Homo sapi
666	45	3.4	1464	10	BC008974	BC008974 Mus muscu	739	45	3.4	1870	9	AB048881	Macaca fa
667	45	3.4	1471	9	BC018762	BC018762 Homo sapi	740	45	3.4	1873	17	AF119859	AF119859 Homo sapi
668	45	3.4	1481	10	BC049618	BC049618 Mus muscu	741	45	3.4	1876	10	BC053422	Mus muscu
669	45	3.4	1501	10	BC020094	BC020094 Mus muscu	742	45	3.4	1879	9	HSN801116	AL117583 Homo sapi
670	45	3.4	1511	10	BC026543	BC026543 Mus muscu	743	45	3.4	1881	9	HSR420545	AJ420545 Homo sapi
671	45	3.4	1522	10	BC027442	BC027442 Mus muscu	744	45	3.4	1886	9	AK025084	AY051798 Drosophila
672	45	3.4	1523	17	AF116614	AF116614 Homo sapi	745	45	3.4	1892	3	AY051798	AY051798 Drosophila
673	45	3.4	1528	9	BC042956	BC042956 Homo sapi	746	45	3.4	1906	9	AB071106	AB071106 Macaca fa
674	45	3.4	1534	9	BC008416	BC008416 Homo sapi	747	45	3.4	1909	10	BC040747	BC040747 Mus muscu
675	45	3.4	1539	10	BC053448	BC053448 Mus muscu	748	45	3.4	1913	10	BC003999	BC003999 Mus muscu
676	45	3.4	1541	3	AK115753	AK115753 Clona int	749	45	3.4	1938	9	BC043555	BC043555 Homo sapi
677	45	3.4	1552	10	BC026370	BC026370 Mus muscu	750	45	3.4	1946	5	BC053207	BC053207 Danio rer
678	45	3.4	1552	9	BC035572	BC035572 Homo sapi	751	45	3.4	1948	9	AK026687	AK026687 Homo sapi
679	45	3.4	1573	3	LVU250884	AJ250884 Loligo vu	752	45	3.4	1948	9	BC044241	Homo sapi
680	45	3.4	1580	9	BC053599	BC053599 Homo sapi	753	45	3.4	1959	9	BC040005	Homo sapi
681	45	3.4	1583	9	BC029035	BC029035 Homo sapi	754	45	3.4	1977	9	AB056792	Macaca fa
682	45	3.4	1592	8	AF019630	AF019630 Magnaport	755	45	3.4	1981	3	AY070835	Drosophila
683	45	3.4	1595	9	BC040734	BC040734 Homo sapi	756	45	3.4	1985	8	AF157059	AF157059 Artemisia
684	45	3.4	1606	10	BC051117	BC051117 Mus muscu	757	45	3.4	1998	9	AB093636	AB093636 Macaca fa
685	45	3.4	1616	10	BC010327	BC010327 Mus muscu	758	45	3.4	2009	5	BC044124	Xenopus l
686	45	3.4	1628	3	AY118763	AY118763 Drosophila	759	45	3.4	2019	3	AY058686	AY058686 Drosophila
687	45	3.4	1630	9	BC039130	BC039130 Homo sapi	760	45	3.4	2019	9	BC004920	Homo sapi
688	45	3.4	1640	9	AB070034	AB070034 Macaca fa	761	45	3.4	2022	10	BC004646	Mus muscu
689	45	3.4	1642	10	BC014817	BC014817 Mus muscu	762	45	3.4	2023	3	AY119490	AY119490 Drosophila
690	45	3.4	1654	3	BRPCHIT	M73689 Bruglia mala	763	45	3.4	2031	6	IMPFTHROM	IMPFTHROM
691	45	3.4	1657	6	EL1332	EL1332 Human cDNA	764	45	3.4	2035	6	IO8608	IO8608
692	45	3.4	1659	6	AX237691	AX237691 Sequence	765	45	3.4	2067	9	BC008732	BC008732 Homo sapi
693	45	3.4	1659	9	HUMP57B	D44497 Human mRNA	766	45	3.4	2073	9	HSN801468	HSN801468
694	45	3.4	1661	10	AF081366	AF081366 Rattus no	767	45	3.4	2080	10	HSN8013564	HSN8013564
695	45	3.4	1664	9	BC028227	BC028227 Homo sapi	768	45	3.4	2096	9	BC050272	BC050272 Homo sapi
696	45	3.4	1664	9	BC041446	BC041446 Homo sapi	769	45	3.4	2098	9	BC011820	Homo sapi
697	45	3.4	1673	10	BC010324	BC010324 Mus muscu	770	45	3.4	2115	9	BC018318	Homo sapi
698	45	3.4	1679	9	BC033143	BC033143 Homo sapi	771	45	3.4	2150	6	AX210648	Sequence
699	45	3.4	1688	9	BC000115	BC000115 Homo sapi	772	45	3.4	2150	9	AF017790	AF017790 Homo sapi
700	45	3.4	1709	9	BC039890	BC039890 Homo sapi	773	45	3.4	2151	10	BC027381	BC027381 Mus muscu
701	45	3.4	1711	6	BD063242	BD063242 Secreted	774	45	3.4	2173	10	BC048927	BC048927 Mus muscu
702	45	3.4	1712	5	BC049516	BC049516 Danio rer	775	45	3.4	2176	10	BC034399	BC034399 Mus muscu
703	45	3.4	1724	9	BC002454	BC002454 Homo sapi	776	45	3.4	2180	9	BC035809	BC035809 Homo sapi
704	45	3.4	1728	6	AR117141	AR117141 Sequence	777	45	3.4	2187	10	BC046283	Mus muscu
705	45	3.4	1728	6	AR254116	AR254116 Sequence	778	45	3.4	2198	9	HSN803382	HSN803382
706	45	3.4	1728	6	BD023469	BD023469 Isolated	779	45	3.4	2227	9	BC004934	Homo sapi
707	45	3.4	1728	9	AF013249	AF013249 Homo sapi	780	45	3.4	2227	9	BC050571	Homo sapi
708	45	3.4	1729	9	BC039813	BC039813 Homo sapi	781	45	3.4	2229	9	HSN803552	HSN803552
709	45	3.4	1732	3	AY118611	AY118611 Drosophila	782	45	3.4	2240	4	AB042653	Bos tauru
710	45	3.4	1746	5	BC052142	BC052142 Danio rer	783	45	3.4	2240	9	BC034937	BC034937 Homo sapi
711	45	3.4	1763	9	BC041473	BC041473 Homo sapi	784	45	3.4	2245	9	BC028076	BC028076 Homo sapi
712	45	3.4	1764	3	AY069232	AY069232 Drosophila	785	45	3.4	2246	9	BC051820	BC051820 Homo sapi
713	45	3.4	1767	3	AY069170	AY069170 Drosophila	786	45	3.4	2249	10	BC024533	BC024533
714	45	3.4	1771	3	AK116800	AK116800 Clona int	787	45	3.4	2255	3	AY089465	AY089465 Drosophila
715	45	3.4	1773	9	BC037559	BC037559 Homo sapi	788	45	3.4	2260	6	BD021751	BD021751 Novel gen
716	45	3.4	1776	5	BC045989	BC045989 Danio rer	789	45	3.4	2260	6	BD083722	BD083722 Nucleic a
717	45	3.4	1776	6	AR099768	AR099768 Sequence	790	45	3.4	2260	6	BD097369	BD097369 Nucleic a
718	45	3.4	1776	6	AR202548	AR202548 Sequence	791	45	3.4	2260	6	BD101689	BD101689 Novel gen
719	45	3.4	1776	6	AR213184	AR213184 Sequence	792	45	3.4	2293	9	BC043566	BC043566 Homo sapi
720	45	3.4	1776	8	NTU38446	U38446 Nicotiana t	793	45	3.4	2296	9	BC013573	BC013573 Homo sapi
721	45	3.4	1782	10	BC050802	BC050802 Mus muscu	794	45	3.4	2296	9	BC044946	BC044946 Homo sapi
722	45	3.4	1788	9	BC042092	BC042092 Homo sapi	795	45	3.4	2313	9	AB070026	AB070026 Macaca fa

796	45	3.4	2326	6	AX351139	Sequence	869	45	3.4	3338	9	HSW803696	AL832388 Homo sapi
797	45	3.4	2353	5	BC053415	Danio rer	870	45	3.4	3382	10	BC031718	BC031718 Mus muscu
798	45	3.4	2356	10	BC050243	Mus muscu	871	45	3.4	3386	9	BC004191	BC004191 Homo sapi
799	45	3.4	2367	9	HSW801757	Sequence	872	45	3.4	3393	6	AX167242	AX167242 Sequence
800	45	3.4	2372	9	BC042652	Mus muscu	873	45	3.4	3404	5	BC044703	BC044703 Xenopus l
801	45	3.4	2373	10	BC031543	Mus muscu	874	45	3.4	3406	9	BC048287	BC048287 Homo sapi
802	45	3.4	2388	9	AF115511	Mus muscu	875	45	3.4	3415	10	AF361078	AF361078 Mus muscu
803	45	3.4	2411	9	BC007420	Homo sapi	876	45	3.4	3420	9	BC038433	BC038433 Homo sapi
804	45	3.4	2416	9	BC032427	Homo sapi	877	45	3.4	3423	10	BC010717	BC010717 Mus muscu
805	45	3.4	2432	10	BC050110	Mus muscu	878	45	3.4	3448	10	BC046596	BC046596 Mus muscu
806	45	3.4	2443	9	BC011658	Mus muscu	879	45	3.4	3500	9	BC030133	BC030133 Homo sapi
807	45	3.4	2445	9	BC019562	Homo sapi	880	45	3.4	3503	10	BC042490	BC042490 Mus muscu
808	45	3.4	2466	10	BC040745	Mus muscu	881	45	3.4	3552	9	BC036784	BC036784 Homo sapi
809	45	3.4	2476	3	AY058712	Drosophila	882	45	3.4	3554	10	AF137367	AF137367 Mus muscu
810	45	3.4	2486	9	BC027910	Homo sapi	883	45	3.4	3566	9	HSW803611	AL832304 Homo sapi
811	45	3.4	2508	5	LFT308118	Lampetra	884	45	3.4	3616	9	HSW804663	AL833350 Homo sapi
812	45	3.4	2516	10	BC037388	Mus muscu	885	45	3.4	3717	3	AF384164	AF384164 Manduca s
813	45	3.4	2522	10	BC049158	Mus muscu	886	45	3.4	3724	9	HSW804529	AL833218 Homo sapi
814	45	3.4	2528	8	AF126550	Glycine m	887	45	3.4	3748	9	BC027942	BC027942 Homo sapi
815	45	3.4	2543	3	AY070710	Drosophila	888	45	3.4	3766	9	HSW800878	AL110222 Homo sapi
816	45	3.4	2543	9	BC003656	Homo sapi	889	45	3.4	3780	10	BC052316	BC052316 Mus muscu
817	45	3.4	2581	3	DDIGP138A	Drosophila	890	45	3.4	3848	9	BC032401	BC032401 Homo sapi
818	45	3.4	2581	10	BC026392	Mus muscu	891	45	3.4	3856	9	HSW805531	AL834437 Homo sapi
819	45	3.4	2606	10	BC023316	Mus muscu	892	45	3.4	3888	10	BC052637	BC052637 Mus muscu
820	45	3.4	2628	9	BC032691	Homo sapi	893	45	3.4	3939	9	BC042431	BC042431 Homo sapi
821	45	3.4	2665	9	BC006136	Homo sapi	894	45	3.4	3988	10	AB029066	AB029066 Mus muscu
822	45	3.4	2668	5	SSA293335	Salmo sal	895	45	3.4	4097	10	BC025565	BC025565 Mus muscu
823	45	3.4	2679	9	BC008198	Homo sapi	896	45	3.4	4106	3	AY128421	AY128421 Drosophila
824	45	3.4	2682	9	BC002473	Homo sapi	897	45	3.4	4115	6	BD012818	BD012818 Ys68, a n
825	45	3.4	2683	10	BC052924	Mus muscu	898	45	3.4	4115	6	BD012822	BD012822 Ys68, a n
826	45	3.4	2685	9	HSW803071	Mus muscu	899	45	3.4	4115	6	BD123392	BD123392 Ys68 gene
827	45	3.4	2687	3	DME312133	Drosophila	900	45	3.4	4115	6	BD123396	BD123396 Ys68 gene
828	45	3.4	2687	9	BC028933	Homo sapi	901	45	3.4	4158	9	BC050289	BC050289 Homo sapi
829	45	3.4	2688	9	BC021087	Homo sapi	902	45	3.4	4165	9	HSW804627	AL833344 Homo sapi
830	45	3.4	2690	9	BC011891	Homo sapi	903	45	3.4	4343	5	AF159906	AF159906 Lapeinis h
831	45	3.4	2719	9	BC012479	Homo sapi	904	45	3.4	4355	10	BC053033	BC053033 Mus muscu
832	45	3.4	2728	9	BC022218	Homo sapi	905	45	3.4	4365	6	AX352580	AX352580 Sequence
833	45	3.4	2733	9	BC041092	Homo sapi	906	45	3.4	4365	6	AX700120	AX700120 Sequence
834	45	3.4	2763	9	AC095553	Homo sapi	907	45	3.4	4365	10	AF114168	AF114168 Mus muscu
835	45	3.4	2776	10	AB076079	Mus muscu	908	45	3.4	4463	10	BC018533	BC018533 Mus muscu
836	45	3.4	2783	10	BC039183	Mus muscu	909	45	3.4	4751	3	AF134171	AF134171 Dictyoste
837	45	3.4	2804	10	S69407	Edg-endogli	910	45	3.4	4820	10	BC052716	BC052716 Mus muscu
838	45	3.4	2815	9	BC001790	Homo sapi	911	45	3.4	4879	5	BC047162	BC047162 Xenopus l
839	45	3.4	2815	9	BC018727	Homo sapi	912	45	3.4	5012	3	AY069824	AY069824 Drosophila
840	45	3.4	2836	6	AR170129	Sequence	913	45	3.4	5076	9	AB062750	AB062750 Homo sapi
841	45	3.4	2836	6	AR170130	Sequence	914	45	3.4	5078	10	BC052172	BC052172 Mus muscu
842	45	3.4	2836	6	BD069549	Novel car	915	45	3.4	5840	9	BC035609	BC035609 Homo sapi
843	45	3.4	2836	6	BD069550	Novel car	916	45	3.4	6157	6	AX344221	AX344221 Sequence
844	45	3.4	2836	9	BC006575	Homo sapi	917	45	3.4	6157	6	AX348614	AX348614 Sequence
845	45	3.4	2840	10	BC052769	Mus muscu	918	45	3.4	6674	10	AB029291	AB029291 Mus muscu
846	45	3.4	2850	9	BC034737	Homo sapi	919	45	3.4	6702	9	AF378756	AF378756 Homo sapi
847	45	3.4	2884	9	HSW800612	Homo sapi	920	45	3.4	6931	9	HSW803520	AL832213 Homo sapi
848	45	3.4	2887	9	AF100752	Homo sapi	921	45	3.4	7034	6	BD012825	BD012825 Ys68, a n
849	45	3.4	2887	9	BC020217	Homo sapi	922	45	3.4	7034	6	BD123399	BD123399 Ys68 gene
850	45	3.4	2894	10	BC051982	Mus muscu	923	45	3.4	7353	10	AB059278	AB059278 Mus muscu
851	45	3.4	2899	9	HSW800643	Homo sapi	924	45	3.4	7536	6	AX346366	AX346366 Sequence
852	45	3.4	2911	9	BC020264	Homo sapi	925	45	3.4	1403	3	AC116959	AC116959 Dictyoste
853	45	3.4	2937	9	BC008857	Homo sapi	926	45	3.4	18567	2	AC018319	AC018319 Drosophila
854	45	3.4	2973	10	BC006077	Mus muscu	927	45	3.4	33569	3	AC115685	AC115685 Dictyoste
855	45	3.4	3014	9	BC024695	Homo sapi	928	45	3.4	36188	3	AC115608	AC115608 Dictyoste
856	45	3.4	3036	9	AF090896	Homo sapi	929	45	3.4	40753	3	BFY18367	Y18367 Branchiosto
857	45	3.4	3042	3	AY069826	Drosophila	930	45	3.4	44621	9	AP001873	AP001873 Homo sapi
858	45	3.4	3137	9	BC000235	Homo sapi	931	45	3.4	47340	9	AC069387	AC069387 Homo sapi
859	45	3.4	3149	10	BC040763	Mus muscu	932	45	3.4	48876	10	AL928841	AL928841 Mouse DNA
860	45	3.4	3157	10	BC037118	Mus muscu	933	45	3.4	49306	3	AC115606	AC115606 Dictyoste
861	45	3.4	3178	9	HSW802265	Homo sapi	934	45	3.4	56028	2	AC101223	AC101223 Mus muscu
862	45	3.4	3179	9	BC018509	Homo sapi	935	45	3.4	57538	3	AL115682	AL115682 Dictyoste
863	45	3.4	3183	9	BC044242	Homo sapi	936	45	3.4	60648	5	AL672044	AL672044 Zebratish
864	45	3.4	3241	3	AY121624	Drosophila	937	45	3.4	64707	3	AC115607	AC115607 Dictyoste
865	45	3.4	3266	9	BC040945	Homo sapi	938	45	3.4	66877	2	AC116062	AC116062 Rattus no
866	45	3.4	3299	9	BC038294	Homo sapi	939	45	3.4	67632	2	AC105102	AC105102 Homo sapi
867	45	3.4	3301	10	BC029098	Mus muscu	940	45	3.4	69966	9	AL391804	AL391804 Human DNA
868	45	3.4	3327	9	HSW805349	Homo sapi	941	45	3.4	72461	9	AC073322	AC073322 Homo sapi

942	45	3.4	79594	9	AL138805	Human DNA
943	45	3.4	88526	10	AL807759	Mouse DNA
944	45	3.4	89222	8	NC18F11	Neurospor
945	45	3.4	90051	10	AL928853	Mouse DNA
946	45	3.4	90373	3	AC115579	Dictyoste
947	45	3.4	90763	8	NCB10H4	Neurospor
948	45	3.4	95548	2	AC129940_3	Continuation (4 of
949	45	3.4	98908	9	AL139279	Human DNA
950	45	3.4	100000	9	AP000208	Homo sapi
951	45	3.4	103308	9	AC092491	Homo sapi
952	45	3.4	105682	3	AC116957_3	Continuation (4 of
953	45	3.4	106664	10	AF130357	Mus muscu
954	45	3.4	106787	10	AL844483	Human DNA
955	45	3.4	107135	9	HS145B12	Human DNA
956	45	3.4	109637	9	HSJ842K24	Human DNA
957	45	3.4	110000	2	AC117022_3	Continuation (4 of
958	45	3.4	110000	2	AC142269_2	Continuation (3 of
959	45	3.4	110000	2	EX284615_0	Mus muscu
960	45	3.4	110000	2	PFMAL6P1_10	Continuation (11 o
961	45	3.4	110000	3	PFMAL8P1_08	Continuation (9 of
962	45	3.4	110000	3	AC116305_2	Continuation (3 of
963	45	3.4	110000	3	AC116984_2	Continuation (3 of
964	45	3.4	113919	9	AP000247	Homo sapi
965	45	3.4	114854	10	AC124211	Mus muscu
966	45	3.4	119575	2	AC142698	Macaca mu
967	45	3.4	119903	9	AC091866	Homo sapi
968	45	3.4	120045	9	AL353052	Human DNA
969	45	3.4	123627	10	AL732428	Mouse DNA
970	45	3.4	124174	10	AL592482	Mouse DNA
971	45	3.4	125914	9	AC114981	Homo sapi
972	45	3.4	125958	3	AC115592	Dictyoste
973	45	3.4	127243	9	AL359545	Human DNA
974	45	3.4	128428	9	AF241730	Homo sapi
975	45	3.4	129306	8	NCB24N11	Neurospor
976	45	3.4	131189	2	AC101756	Mus muscu
977	45	3.4	131189	2	AC101756	Mus muscu
978	45	3.4	132254	3	AC116330	Dictyoste
979	45	3.4	132254	3	AC116330	Dictyoste
980	45	3.4	132254	3	AC116330	Dictyoste
981	45	3.4	134016	2	AC048388	Homo sapi
982	45	3.4	135218	2	AC119026	Rattus no
983	45	3.4	136365	9	AC011413	Homo sapi
984	45	3.4	136493	2	AC069001	Homo sapi
985	45	3.4	142025	2	AC137541	Felis cat
986	45	3.4	143177	9	CNS01DW5	Human chr
987	45	3.4	143928	10	AC142473	Mus muscu
988	45	3.4	143929	10	AC142473	Mus muscu
989	45	3.4	144195	10	AL935297	Mouse DNA
990	45	3.4	144854	10	AL670758	Mouse DNA
991	45	3.4	145443	10	AL645824	Mouse DNA
992	45	3.4	145630	2	AC114680	Mus muscu
993	45	3.4	146948	10	AL833785	Mouse DNA
994	45	3.4	147392	5	AL627261	Zebrafish
995	45	3.4	147501	2	CNS0364R	Oryza sat
996	45	3.4	150734	2	AL139117	Homo sapi
997	45	3.4	151023	9	AC087342	Homo sapi
998	45	3.4	151457	8	AP003410	Oryza sat
999	45	3.4	151802	3	AC114263	Dictyoste
1000	45	3.4	152289	9	AC087430	Homo sapi

ALIGNMENTS

RESULT 1	AR204971	Sequence 67 from patent US 6368828.	linear	PAT 20-JUN-2002
LOCUS	AR204971	3375 bp	DNA	
DEFINITION	AR204971			
ACCESSION	AR204971			
VERSION	AR204971.1	GI:21502434		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			

REFERENCE	1 (bases 1 to 3375)	Unclassified.
AUTHORS	Laroche, W., Patel, B.K.R. and Pierce, J.H.	
TITLE	Attenuated and dominant negative variant cDNAs of Stat6: Stat6b and Stat6c	
JOURNAL	Patent: US 6368828-A 67 09-APR-2002;	
FEATURES	Location/Qualifiers	
source	1..3375	
BASE COUNT	799 a 969 c 948 g 659 t	
ORIGIN		
Query Match	3.8%; Score 50; DB 6; Length 3375;	
Best Local Similarity	100.0%; Pred. No. 4.7e-17;	
Matches	50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Cy	1277 TTCGTGTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326	
Db	3318 TTCGTGTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3367	
RESULT 2		
LOCUS	AB065088	677 bp mRNA linear PRI 23-MAY-2002
DEFINITION	Homo sapiens OK/KNS-cl.6 mRNA for ribosomal protein S2, complete cds.	
ACCESSION	AB065088	
VERSION	AB065088.1	GI:21104509
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1	
AUTHORS	Nonaka, Y., Shichijo, S. and Itoh, K.	
TITLE	Genes encoded epitopes recognized by CTL established from TIL of colon cancer	
JOURNAL	Published Only in Database (2002)	
REFERENCE	2 (bases 1 to 677)	
AUTHORS	Itoh, K. and Shichijo, S.	
TITLE	Direct Submission	
JOURNAL	Submitted (06-JUL-2001) Shigeaki Shichijo, Kurume University School of Medicine, Department of Immunology; 67 Asahi-machi, Kurume, Fukuoka 830-0011, Japan (E-mail: shichijo@med.kurume-u.ac.jp, Tel: 81942337551, Fax: 81942337699)	
FEATURES	Location/Qualifiers	
source	1..677	
gene	/organism="Homo sapiens"	
CDS	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/cell_line="KNS60"	
	/cell_type="malignant glioma"	
	1..677	
	/genes="OK/KNS-cl.6"	
	310..549	
	/genes="OK/KNS-cl.6"	
	/codon_start=1	
	/product="ribosomal protein S2"	
	/protein_id="BAB93525.1"	
	/db_xref="GI:21104510"	
	/translation="MMAGIDDCYTSARGCTATLGNFAKATFADSAISKTSYLTPLDWKE TVFTKSPYOEFTHLVKTHTRVSVQTPAVATT"	
BASE COUNT	217 a 186 c 155 g 119 t	
ORIGIN		
Query Match	3.6%; Score 48; DB 9; Length 677;	
Best Local Similarity	100.0%; Pred. No. 5.7e-16;	
Matches	48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Cy	1279 CGTGTAAAAA 1326	
Db	583 CGTGTAAAAA 630	

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RESULT 3
AY069529
LOCUS
DEFINITION Drosophila melanogaster LD24634 full insert cDNA.
ACCESSION AY069529
VERSION AY069529.1 GI:17862393
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1210)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J.,
Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K.,
Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
Direct Submission
Submitted (10-DEC-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
2 (bases 1 to 1210)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Drensek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
and Celniker, S.
Direct Submission
Submitted (22-JAN-2003) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu.
Location/Qualifiers
1. .1210
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
1. .1210
/gene="dbe"
/db_xref="FLYBASE:FBgn020305"
60. .1097
/gene="dbe"
/notes="Longest ORF"
/codon_start=1
/product="LD24634p"
/protein_id="AAL39674.1"
/db_xref="GI:17862394"
/db_xref="FLYBASE:FBgn020305"
/translations="MSESAEETKISTEPVDNAWMKIPAFROEDPHGWEVSSPAT
LFPKYRERYLKEVWPLVEOCLAELHLKAEIDLMEGSMVVKTSKTDWDPVILIKARDMI
KLMSRVPEQAKEVLQDDIGCDIILKGLVHKKEKVRQELIGPNATLKSIELL
TDCVTVQGNVTVSALGPYKGLQOVRDVLVETMNNVHTPIYTKALMIKRELMKDPRLAN
EDWSEFLPKPKNKINISKEQPKVKQKQKVEYTFEPSPQESKVDKQLASGEVLANOEOK
QAKRQKERTKEKAAKQDERRNKDFVPPTESAAASKKEDGSSSKVDVKALKAK
LIKANKKARSS"
BASE COUNT 379 a 287 c 336 g 208 t
ORIGIN
Query Match 3.6%; Score 48; DB 3; Length 1210;
Best Local Similarity 100.0%; Pred. No. 6.1e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1279 CQTGTAAAAA 1326
Db 1161 CQTGTAAAAA 1208
RESULT 4
AY153819
LOCUS
DEFINITION Sequence 1 from patent US 6235972.
ACCESSION AR153819
VERSION AR153819.1 GI:15121351
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1522)
AUTHORS Mahajan, P.B. and Tagliani, L.
TITLE Maize Rad23 genes and uses thereof
JOURNAL Patent: US 6235972-A 1 22-MAY-2001;
FEATURES
Location/Qualifiers
source
1. .1522
/organism="unknown"
BASE COUNT 430 a 375 c 370 g 347 t
ORIGIN
Query Match 3.6%; Score 48; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 6.2e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1279 CQTGTAAAAA 1326
Db 1455 CQTGTAAAAA 1502
RESULT 5
AR243792
LOCUS
DEFINITION Sequence 30 from patent US 6476195.
ACCESSION AR243792
VERSION AR243792.1 GI:27291285
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 2227)
AUTHORS Komatsoulis, G., Rosen, C.A., Ruben, S.M., Duan, R.D., Moore, P.A.,
Shi, Y., Lafleur, D.W., Wei, Y.-F., Ni, J., Florence, K.A., Young, P.,
Brewer, L.A., Soppet, D.R., Endress, G.A., Ebner, R., Olsen, H. and
Mucenski, M.
TITLE Secreted protein HNFGF20
JOURNAL Patent: US 6476195-A 30 05-NOV-2002;
FEATURES
Location/Qualifiers
source
1. .2227
/organism="unknown"
BASE COUNT 544 a 539 c 553 g 21 others
ORIGIN
Query Match 3.6%; Score 48; DB 6; Length 2227;
Best Local Similarity 100.0%; Pred. No. 6.5e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1279 CQTGTAAAAA 1326
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Blakesley,R.W., Bouffard,G.G., Breen,X., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantipop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.B., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAP Kit: 55 Row: h Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

Location/Qualifiers

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1. .2969
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5346773"
/tissue_type="mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI CGAP_Mam6"
/lab_host="DH105"
/notes="Vector: pCMV-SPORT6"
<1. .2969
/gene="Nr1d1"
/notes="synonyms: MGC25477, 2600011106Rik, NRD-C"
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gene

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/db_xref="LocustID:230598"
/db_xref="MGI:1201386"
<1. .2892
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/product="Nr1d1 protein"
/protein_id="AAH23786.1"
/db_xref="GI:23271734"
/db_xref="LocustID:230598"
/db_xref="MGI:1201386"
/translation="PRVLRVGRVGDPRVKRTKQSAALCVGVSGFADPDLLGL
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CDS

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AFLEHMFWSGLKYDEVEAVDSYQLARPSPDANKRMLFGSLARPQHPMGKFWGN
WAQFFTHPLMIRDAIDREAVDSYQLARPSPDANKRMLFGSLARPQHPMGKFWGN
AETLKEPKKNIDTHARLEFWMRYSHAYMTLVQSKETLDTLEKVTETPSQIPN
NGLPKFNSHLTDPFPAPKQYRVVPIRKIKHALTITWALPPQQQRYNKPILYISV
LVGHEGKGSILSYLRKKWALALFGNGETGFQNSTYSVFSITLDTGEVHFYEV
ATVTFQYLMQXLPKEKRVFEIQIEDNEFYQRTDPVEYVENMCMQYPRQD
FTGDDLLPKPYKEVIAEALNOLVPOKANLVLSGANEGRCDLKEKWFQYQYSIEDIE
NSWTEKLPNFDLPDLHPAENKYIATDFLKAFCPEYEPYPAKIVTQAGCLWYK
DNKEFKPVARFHLISPLQKSAANVLFDFIVNLTNLAEPYEAADVQALEYKLV
AGEHGLIIRVGNHKLPLLFQIILDIYLFSTPAVFTMTQLKTYFNILIKPET
LAKDVRLLILEYRSWMDIKYQALMDGLSDLSLINFVKQSFQVGLVQGNVTSTE
SMDPLKYVDKLNFALEMEPCFPQVVELPSGHILCKPRAALNGDANSEVTVYQSG
TRSLREYTMELLVMMEEPCFPQVVELPSGHILCKPRAALNGDANSEVTVYQSG
YNSBETVDKTEEFELSPSEKIEMLTDAFNQVYPTCRNTSGILGFSVTGQATK
VTCQYLDRLAHIEALKSPSKSLDSVSWFKAHKPGSKMLSVHVGVGKYLEEDGAP
FGDSNSRGQQLTYLPPSPVLAESTYPTIDTIDRAFTLSLFFYHKIVK"
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BASE COUNT 869 a 654 c 681 g 765 t

Query Match 3.6%; Score 48; DB 10; Length 2969;
Best Local Similarity 100.0%; Pred. No. 6.7e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1279 CGTGTAACAAAAA 1326

Db 2919 CGTGTAACAAAAA 2966

RESULT 8
AX203306
LOCUS
DEFINITION Sequence 51 from Patent WO0153836.
ACCESSION AX203306

VERSION AX203306.1 GI:15392677

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Schlegel,R., Endege,W. and Monahan,J.E.
Identification, assessment, prevention, and therapy of prostate cancer

AUTHORS

Patent: WO 0153836-A 51 26-JUL-2001;

JOURNAL

Millennium Predictive Medicine, Inc. (US)

FEATURES

source

1. .112
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606" 16 t

BASE COUNT

78 a 5 c 13 g 16 t

ORIGIN

Query Match 3.5%; Score 47; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAACAAAAA 1326

Db 47 GTGTAACAAAAA 93

RESULT 9

PSGAMRA

LOCUS

P.sativum GA mRNA (clone A).

DEFINITION

X65154

ACCESSION

X65154.1 GI:20724

VERSION

KEYWORDS

SOURCE

ORGANISM

Pisum sativum (pea)

Pisum sativum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.

1 (bases 1 to 575)

Cohn,N.S., Zhang,L., Mitchell,J.P. and Vierheller,C.Z.

Gibberellin-stimulated changes in abundance of two mRNAs in the
developing shoot of dwarf peas (*Pisum sativum* L.)

Int. J. Plant Sci. 155, 498-505 (1994)

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (25-MAR-1992) N.S. Cohn, Ohio University, Dept of Botany,
Athens, Ohio 45701, USA

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (26-JAN-1993) N.S. Cohn, Ohio University, Dept of Botany,
Athens, Ohio 45701, USA

REMARK

FEATURES

source

1. .575
/organism="Pisum sativum"
/mol_type="mRNA"
/strain="Little Marvel"
/db_xref="taxon:3888"
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/haplotype="n=7"
/cell_type="stem tissue"
/tissue_type="stem tissue"
/clone_lib="pea cDNA from GA-treated dwarf peas"
/dev_stage="12 day seedlings"
1. .575
/gene="GA"
prim_transcript 3. .525

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24. .452
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/db_xref="SPREMBL:C41016"
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IKVAGNSDPATVNSAFQLEACERFGGACLAIDMTPEVKLOPERSNDAPKTA
SENIDRDYLEYNDPKTVFOAEACDILGGTFCEPDYQGVY"
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227
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BASE COUNT 201 a 129 c 104 g 141 t
ORIGIN
Query Match 3.5%; Score 47; DB 8; Length 575;
Best Local Similarity 100.0%; Pred. No. 2.1e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1280 GTGTAACAAAAA 1326
Db 522 GTGTAACAAAAA 568
RESULT 10
AF467914 679 bp mRNA linear VRT 02-FEB-2003
LOCUS
DEFINITION Danio rerio parvalbumin isoform 1d mRNA, complete cds.
ACCESSION AF467914
VERSION AF467914.1 GI:28194097
KEYWORDS
SOURCE Danio rerio (zebrafish)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 679)
Hsiao,C.D., Tsai,W.Y. and Tsai,H.J.
Molecular cloning and developmental expression of parvalbumin genes
in zebrafish
Unpublished
2 (bases 1 to 679)
Hsiao,C.D., Tsai,W.Y. and Tsai,H.J.
Direct Submission
Submitted (15-JAN-2002) Institute of Fisheries Science, 1 Roosevelt
Rd. 4 Sec. National Taiwan University, Taipei 106, Taiwan
FEATURES
source
1. .679
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
28. .357
/note="Ca2+ buffer; pvalb1d"
/codon_start=1
/product="parvalbumin isoform 1d"
/protein_id="AAO33400.1"
/db_xref="GI:28194098"
/translation="MAVGALIAADVDAAALAAQAAADFDYKSPFAKVGLSAKSADEV
KKAPAIIDODNSGFIEBELKFLQNFKANARVLTDKETKAFLSAGSDGDKIGAE
FAALVKA"
BASE COUNT 208 a 151 c 153 g 167 t
ORIGIN
Query Match 3.5%; Score 47; DB 5; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1280 GTGTAACAAAAA 1326
Db 619 GTGTAACAAAAA 665
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RESULT 11
I03321 688 bp ss-DNA linear PAT 21-MAY-1993
LOCUS
DEFINITION Sequence 12 from Patent US 4886747.
ACCESSION I03321
VERSION I03321.1 GI:270715
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 688)
Derynck,R.M.A. and Goeddel,D.V.
Nucleic acid encoding TGF-beta, and its uses
Patent: US 4886747-A 12-DEC-1989;
Genentech, Inc.; South San Francisco, CA
FEATURES
Location/Qualifiers
source
1. .688
/organism="unknown"
BASE COUNT 240 a 137 c 138 g 173 t
ORIGIN
Query Match 3.5%; Score 47; DB 6; Length 688;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1280 GTGTAACAAAAA 1326
Db 594 GTGTAACAAAAA 640
RESULT 12
BC053374 899 bp mRNA linear PRI 09-JUN-2003
LOCUS
DEFINITION Homo sapiens cDNA clone IMAGE:6169687, partial cds.
ACCESSION BC053374
VERSION BC053374.1 GI:31419639
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 899)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Pahay,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
MEDLINE
12477932
2 (bases 1 to 899)
Strausberg,R.
Direct Submission
TITLE
JOURNAL
AUTHORS
TITLE
JOURNAL
```


REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 115 Row: n Column: 13
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4885570.

FEATURES

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 /db_xref="taxon:9606"
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 /issue_type="Eye, retinoblastoma"
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 /lab_host="DH108"
 /note="Vector: pCMV-SPORT6"
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 Best Local Similarity 100.0%; Pred. No. 2.3e-15;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA
 DB 820 GTGTAAAAA

RESULT 13
 AX478009
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

1
 Cahoon, E.B., Cahoon, R.E., Klein, T.M., Rafalski, A.J. and Sakai, H.
 Floral development genes
 Patent: WO 0244390-A 19 06-JUN-2002;
 E. I. du Pont de Nemours and Company (US)

FEATURES

source
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 /mol_type="genomic DNA"
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QY 1280 GTGTAAAAA
 DB 822 GTGTAAAAA

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 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
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Homo sapiens mRNA full length insert cDNA clone EUROIIMAGE 712308.
 AL079309.1 GI:5102753
 FLX_CDNA.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1
 Auffray, C., Ansorge, W., Ballabio, A., Estivill, X., Gibson, K.,
 Lehrach, H., Poustka, A. and Lundeberg, J.
 The European IMAGE consortium for integrated Molecular analysis of
 human gene transcripts
 Unpublished
 2 (bases 1 to 956)
 Direct Submission
 Submitted (15-JUN-1999) Telethon Institute of Genetics and Medicine
 (TIGEM), Via Olgettina 58, 20132 Milano, ITALY. Tel: ++39-02-215601
 Fax: ++39-02-21560220 WWW site: <http://www.tigem.it> e-mail
 enquires: bassi@tigem.it, borsani@tigem.it
 EURO-IMAGE Consortium Contact: Auffray C
 CNRS UPR 420 - Genetique Moleculaire et Biologie du Developement
 IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8
 94801 Villejuif Cedex, FRANCE
 Tel: ++33-1-49 58 34 98
 Fax: ++33-1-49 58 35 09
 e-mail: auffray@infobiogen.fr
 This clone is available royalty-free through IMAGE Consortium
 Distributors.
 IMPORTANT: This sequence represents the full insert of this IMAGE
 cDNA clone. No attempt has been made to verify whether this
 corresponds to the full-length of the original mRNA from which it
 was derived.

FEATURES
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 /clone_lib="NCI_CGAP_GCB1"
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 Best Local Similarity 100.0%; Pred. No. 2.3e-15;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA
 DB 910 GTGTAAAAA

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 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens, clone IMAGE:5204063, mRNA, partial cds.
 BC027909.1 GI:20379883
 Homo sapiens (human)
 Homo sapiens

BC027909
 Homo sapiens
 Eukaryota; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

BC027909
 Homo sapiens
 Eukaryota; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

BC027909
 Homo sapiens
 Eukaryota; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

BC027909
 Homo sapiens
 Eukaryota; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

BC027909
 Homo sapiens
 Eukaryota; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 981)

Strausberg, R.

Direct Submission

Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgaps@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mgc@nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Lari, P., Legaspi, R., Maduro, Q.L.,

Masiello, C., Maskripop, S., Mastrian, S.D., McCloskey, J.C., McDowell, J.,

Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C.,

Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A.,

Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAX Plate: 49 Row: f Column: 15

This clone was selected for full length sequencing because it

passed the following selection criteria: Hexamer frequency ORF
analysis.

FEATURES

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1. .981

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/lab_host="DH10B"

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/codon_start=2

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BASE COUNT

320 a 248 c 181 g 232 t

ORIGIN

Query Match 3.5%; Score 47; DB 9; Length 981;

Best Local Similarity 100.0%; Pred. No. 2.3e-15;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1280 GTGTAA 1326

Db 880 GTGTAA 926

Search completed: November 7, 2003, 18:41:27

Job time : 5055 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 15:40:45 ; Search time 399 Seconds

(without alignments)

8971.065 Million cell updates/sec

Title: US-10-024-806-1

Perfect score: 1326

Sequence: 1 gcgcggagcttccaaagccc.....aaaaaaaaaaaaaaaaaaaaa 1326

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	50	3.8	3375	20	AA28358 Human Stat5 coding
2	48	3.6	1522	21	AA01230 Maize Rad23 protei
3	48	3.6	2227	21	AA26365 Human secreted pro
4	48	3.6	2227	22	AAH3484 Human colon cancer
5	48	3.6	2227	25	ACCS0729 Human secreted pro
6	48	3.6	2227	25	ABZ71405 Secreted protein-e
7	47	3.5	112	22	NA23329 Human prostate can
8	47	3.5	380	23	ABV58152 Human prostate exp

9	47	3.5	384	23	ABV57927 Human prostate exp
10	47	3.5	429	22	AA19141 Human polynucleoti
11	47	3.5	439	23	ABV48477 Human prostate exp
12	47	3.5	902	24	AA042244 Corn FI homologue
13	47	3.5	939	25	ABX78363 Soybean stress res
14	47	3.5	1015	20	AA000713 Human secreted pro
15	47	3.5	1140	21	AAC59279 Human secreted pro
16	47	3.5	1201	21	AAZ97044 Human secreted pro
17	47	3.5	1371	22	ABA06561 Human cDNA SEQ ID
18	47	3.5	1371	22	ABV83898 Human polynucleoti
19	47	3.5	1428	22	AA040837 cDNA encoding nove
20	47	3.5	1505	25	AA0151962 Human extracellular
21	47	3.5	2057	22	AAF72803 Secreted protein g
22	47	3.5	2639	19	AAV52934 Pig transforming g
23	47	3.5	2669	15	AAQ56925 Pig TGF-beta-3 S
24	47	3.5	2671	11	AAQ03303 Entire porcine tra
25	47	3.5	2676	11	AAQ02819 cDNA sequence enco
26	47	3.5	2968	21	AA078190 Human cancer assoc
27	47	3.5	2968	22	AAH34408 Human colon cancer
28	47	3.5	2968	22	AAF32706 Human secreted pro
29	47	3.5	4186	20	AAZ41320 Human normal ovari
30	46	3.5	194	23	ABV48180 Human prostate exp
31	46	3.5	198	23	ABV56955 Human prostate exp
32	46	3.5	211	23	ABV59290 Human prostate exp
33	46	3.5	223	23	ABV57510 Human prostate exp
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36	46	3.5	287	22	AA024917 Bovine ESR associa
37	46	3.5	292	25	ABX47011 Human prostate exp
38	46	3.5	309	23	ABV56871 Human prostate exp
39	46	3.5	317	25	ABX38201 Bovine ESR associa
40	46	3.5	347	13	AAQ27482 T23 cDNA. Oryza s
41	46	3.5	357	23	ABV56577 Human prostate exp
42	46	3.5	358	22	AAK63837 Human immune/haema
43	46	3.5	371	22	AA182880 Human polynucleoti
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45	46	3.5	383	25	ABX40401 Bovine ESR associa
46	46	3.5	392	23	ABV48356 Human polynucleoti
47	46	3.5	401	22	AA187524 Human prostate exp
48	46	3.5	403	22	AA187330 Human polynucleoti
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50	46	3.5	411	22	AA191834 Human polynucleoti
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56	46	3.5	439	23	ABV57512 Human prostate exp
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66	46	3.5	567	22	AA089704 Human prostate exp
67	46	3.5	586	23	ABV56303 Human colon cancer
68	46	3.5	593	21	AA016257 Clone H905.107. H
69	46	3.5	742	18	AAV00437 Human secreted pro
70	46	3.5	743	22	AA023920 Human prostate exp
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72	46	3.5	773	20	AA037388 Human musculoskele
73	46	3.5	773	22	AA026849 Human cDNA encodin
74	46	3.5	773	22	AA016751 Human novel protei
75	46	3.5	773	25	ABX58638 cDNA encoding nove
76	46	3.5	809	21	AAC59304 Human secreted pro
77	46	3.5	809	22	AAH33266 Human colon cancer
78	46	3.5	809	22	ABZ73377 Secreted protein-e
79	46	3.5	809	25	ABZ66985 Human secreted pro
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83	46	3.5	901	24	AB199659	Mouse ischaemic co	156	46	3.5	3281	22	AD08389	Human secreted pro
c 84	46	3.5	951	22	AA526859	Human cDNA encodin	157	46	3.5	3344	16	AAQ80228	Rat NDF clone 22 D
85	46	3.5	1014	21	AA529164	Human secreted pro	158	46	3.5	3376	22	AA560774	Human cancer agent
c 86	46	3.5	1065	25	ABT13321	Breast specific re	159	46	3.5	3436	22	AA500767	Human B7-H3 cDNA c
87	46	3.5	1097	21	AA16195	Human prostate can	160	46	3.5	3436	22	AA500767	Human secreted pro
88	46	3.5	1164	24	AB054448	Human ovarian anti	161	46	3.5	3513	22	AB082683	TRIO like gene SEQ
89	46	3.5	1170	21	AA234331	cDNA encoding huma	162	46	3.5	3513	25	ACC46003	Human TRIO-like ge
90	46	3.5	1218	24	AA45834	Human secreted pro	163	46	3.5	3521	24	ABA96406	Human cacherin fam
c 91	46	3.5	1244	22	AAH33206	Human colon cancer	164	46	3.5	5120	25	ACC44839	Mouse LTPB-4 short
92	46	3.5	1282	24	AA567784	Human receptors an	165	46	3.5	5440	25	ACC44838	Mouse LTPB-4 long
c 93	46	3.5	1542	21	AA966669	DNA encoding a hum	166	46	3.5	6153	22	AAH18670	Human cDNA sequenc
94	46	3.5	1577	21	AA080569	Human secreted pro	167	46	3.5	6410	25	ABZ33706	Human colon tumour
95	46	3.5	1637	24	AA172316	Human transporter	168	46	3.5	6791	18	AA783319	Mouse receptor ME2
96	46	3.5	1660	21	AA297136	Human secreted pro	169	46	3.5	10195	18	AA783320	Mouse receptor ME2
c 97	46	3.5	1699	22	AA781789	Human secreted pro	170	45	3.4	188	24	ABL38026	Human colon tumour
98	46	3.5	1699	25	ACC50677	Human secreted pro	171	45	3.4	190	23	ABV20053	Human prostate exp
99	46	3.5	1757	22	AA78964	Human D-HSP70 cDNA	172	45	3.4	193	22	AAK55174	Human immune/haema
100	46	3.5	1768	22	AA050563	Human secreted pro	173	45	3.4	198	23	ABV56628	Human prostate exp
101	46	3.5	1771	21	AA221662	Human breast and o	174	45	3.4	202	21	AA098563	Human colon cancer
102	46	3.5	1781	20	AA220104	Wheat serine palmi	175	45	3.4	209	23	ABV58765	Human prostate exp
103	46	3.5	1818	24	ABQ54937	Human ovarian anti	176	45	3.4	217	25	ABX30207	Human GDP-mannose
104	46	3.5	1820	20	AA200434	Human secreted pro	177	45	3.4	233	22	AAH31389	Human secreted pro
105	46	3.5	1843	22	AAH33289	Human colon cancer	178	45	3.4	255	25	ABX31005	Human GDP-mannose
106	46	3.5	1844	19	AAV24018	Human BHF1 coding	179	45	3.4	260	23	ABV58104	Human prostate exp
107	46	3.5	1872	24	ABN85798	Human phospholipas	180	45	3.4	272	23	ABV18469	Human prostate exp
108	46	3.5	2002	24	AB544009	Human hydroxymethy	181	45	3.4	274	22	AAH33782	Human colon cancer
109	46	3.5	2002	25	ABX93299	cDNA encoding huma	182	45	3.4	276	25	ABX32152	Human GDP-mannose
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c 111	46	3.5	2029	20	AA219897	Human foetal kidn	184	45	3.4	302	21	AA098700	Human colon cancer
112	46	3.5	2058	21	AA077754	Human cancer assoc	185	45	3.4	304	24	ABQ54969	Human ovarian anti
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114	46	3.5	2087	21	AA077500	Human ORFX ORF3055	187	45	3.4	308	24	ABL62809	Breast cancer rela
115	46	3.5	2112	24	ABX91996	Lung specific nucl	188	45	3.4	308	24	ABL62809	Breast cancer rela
116	46	3.5	2136	21	AA265065	Membrane-bound pro	189	45	3.4	319	23	ABV49812	Human prostate exp
117	46	3.5	2136	22	AA546038	Human DNA encoding	190	45	3.4	332	22	AAH70043	Human prostate exp
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120	46	3.5	2136	25	ABX98268	Human cDNA encodin	193	45	3.4	346	23	ABV54289	Human prostate exp
121	46	3.5	2136	25	ABX98768	Novel human secret	194	45	3.4	365	25	ABX40291	Human prostate exp
122	46	3.5	2136	25	AA05813	Human secreted/tra	195	45	3.4	385	22	AA190964	Bovine EST associa
123	46	3.5	2136	25	ABX97857	Human secreted/tra	196	45	3.4	391	22	AA182408	Human polynucleoti
124	46	3.5	2136	25	ABX80313	Novel human secret	197	45	3.4	395	22	AA187795	Human polynucleoti
125	46	3.5	2136	25	ABX80817	Human secreted/tra	198	45	3.4	399	22	AA188765	Human polynucleoti
126	46	3.5	2136	25	ABX81200	Novel human secret	199	45	3.4	399	23	ABV58210	Human prostate exp
127	46	3.5	2136	25	ABX77901	Human secreted/tra	200	45	3.4	407	23	ABV58185	Human prostate exp
128	46	3.5	2136	25	ABX79029	Human PRO polynucl	201	45	3.4	424	23	ABV55712	Human prostate exp
129	46	3.5	2136	25	ABX78641	Human PRO polynucl	202	45	3.4	426	22	AA188632	Human polynucleoti
130	46	3.5	2136	25	ABX79497	Human secreted/tr	203	45	3.4	443	8	AA070773	Sequence encoding
131	46	3.5	2136	25	ABX75654	Human cDNA encodin	204	45	3.4	444	25	ABX36116	Bovine EST associa
132	46	3.5	2136	25	ABX76859	Human PRO polynucl	205	45	3.4	447	24	ABL93994	Arabidopsis thalia
133	46	3.5	2136	25	ABX64136	cDNA encoding huma	206	45	3.4	452	24	ABV95411	Human pancreatic c
134	46	3.5	2136	25	ABX16699	Human cDNA encodin	207	45	3.4	456	22	AA183054	Human polynucleoti
135	46	3.5	2136	25	ABX17100	Human PRO polynucl	208	45	3.4	456	25	ABX44494	Bovine EST associa
136	46	3.5	2196	19	AAV59663	Human secreted pro	209	45	3.4	462	23	ABV57002	Human prostate exp
137	46	3.5	2196	24	AB573650	Human cDNA #1 for	210	45	3.4	465	23	ABV48253	Human prostate exp
138	46	3.5	2235	22	AA084351	Corn clone CPR951	211	45	3.4	481	23	ABV58614	Human prostate exp
139	46	3.5	2248	21	AA059806	Human secreted pro	212	45	3.4	489	23	ABV23693	Human prostate exp
140	46	3.5	2263	24	AA054413	Human ovarian anti	213	45	3.4	489	23	ABV29562	Human prostate exp
c 141	46	3.5	2360	22	AA077734	Human secreted pro	214	45	3.4	524	21	AA096571	Noncoding region o
142	46	3.5	2457	22	AA033081	DNA encoding huma	215	45	3.4	550	23	ABV57072	Human prostate exp
143	46	3.5	2527	21	AA182234	Lung cancer associ	216	45	3.4	551	23	ABV56917	Human prostate exp
144	46	3.5	2534	22	AA050502	Human secreted pro	217	45	3.4	556	24	ABQ36996	Oligonucleotide fo
145	46	3.5	2611	24	AB576421	cDNA encoding huma	218	45	3.4	556	24	ABQ36997	Oligonucleotide fo
146	46	3.5	2625	21	AAZ91922	Human mahogany pro	219	45	3.4	584	23	ABV57816	Human prostate exp
147	46	3.5	2760	22	AA077710	Human secreted pro	220	45	3.4	595	21	AA081133	Human secreted pro
148	46	3.5	2837	19	AAV46317	Human secreted pro	221	45	3.4	595	22	AA011171	Fertilisation-inde
149	46	3.5	2837	22	AA098483	Human cDNA clone C	222	45	3.4	600	24	ABQ52494	Oligonucleotide fo
150	46	3.5	2892	19	AAV58361	Coding sequence fo	223	45	3.4	600	24	ABQ52495	Oligonucleotide fo
151	46	3.5	2897	19	AAV28411	Human GATA-6 trans	224	45	3.4	601	21	AAZ51740	Glycine max thioe
152	46	3.5	2897	25	AA056565	Human signalling p	225	45	3.4	638	24	ABQ49520	Oligonucleotide fo
153	46	3.5	2924	25	ABT23242	Seed development e	226	45	3.4	638	24	ABQ49521	Oligonucleotide fo
154	46	3.5	2996	24	ABZ58826	Human 32624 polype	227	45	3.4	640	24	ABV83665	Human breast speci

228	45	3.4	690	22	ABH33877	Human colon cancer	301	45	3.4	1436	25	ABX73434	Human novel polynu
229	45	3.4	691	20	AZ52929	Human prostate tum	302	45	3.4	1483	22	AS04152	Human ras converti
230	45	3.4	707	22	AS25840	Human CDNA encodin	303	45	3.4	1492	22	ACC00648	Zea mays oil trait
231	45	3.4	707	22	ABX73181	Human novel polynu	304	45	3.4	1504	24	ABQ54998	Human ovarian anti
232	45	3.4	713	22	AS26603	Human CDNA encodin	305	45	3.4	1507	22	AA05541	Human secreted pro
233	45	3.4	713	22	ABX73944	Human novel polynu	306	45	3.4	1549	20	AA024921	Guman ras carboxy-
234	45	3.4	740	19	AAV23915	Plant CCR enzyme D	307	45	3.4	1556	21	AAC66427	Human secreted pro
235	45	3.4	740	19	AAV23915	Pine cinnamoyl-CoA	308	45	3.4	1583	22	AAH34904	Human colon cancer
236	45	3.4	740	20	AA06881	Pinus radiata CCR	309	45	3.4	1657	17	AAV30360	Human p57 coding s
237	45	3.4	741	19	AAV23878	Plant CCR enzyme D	310	45	3.4	1659	22	AAK34941	Human haematologic
238	45	3.4	741	19	AAV206882	Pine cinnamoyl-CoA	311	45	3.4	1659	24	ABK83666	Human CDNA differe
239	45	3.4	741	21	AA67965	Pinus radiata CCR	312	45	3.4	1686	21	AACT7763	Human cancer assoc
240	45	3.4	756	24	AAH37828	Soybean KCP-like p	313	45	3.4	1694	20	AAH07431	Homo sapiens secre
241	45	3.4	768	24	ABN99158	Arabidopsis thalia	314	45	3.4	1711	19	AAV43617	Human secreted pro
242	45	3.4	775	21	AA61277	Human secreted pro	315	45	3.4	1721	22	AAV63820	Human secreted pro
243	45	3.4	780	21	AAV21763	Human breast and o	316	45	3.4	1728	19	AAV38990	Human receptor for
244	45	3.4	788	21	AA68003	Pinus radiata CCR	317	45	3.4	1767	22	AA529126	CDNA encoding for
245	45	3.4	826	16	AAQ79736	Flower style-speci	318	45	3.4	1767	24	AB568266	CDNA encoding huma
246	45	3.4	826	18	AA764553	Tomato S-ribonucle	319	45	3.4	1776	18	AAAT91744	Tobacco calcium/ca
247	45	3.4	844	22	AA502226	Soybean Wuschel (W	320	45	3.4	1779	21	AAZ65347	Human secreted pro
248	45	3.4	887	21	AA59297	Human secreted pro	321	45	3.4	1797	22	AAI64157	Maize defence-indu
249	45	3.4	895	22	AAH34628	Human colon cancer	322	45	3.4	1800	22	AAV07579	Human secreted pro
250	45	3.4	907	24	ABK52046	CDNA encoding maiz	323	45	3.4	1821	19	AAV59590	Human secreted pro
251	45	3.4	909	21	AAV79961	Human secreted pro	324	45	3.4	1835	20	AAZ27245	Human CLARI coding
252	45	3.4	921	19	AAV40521	Homo sapiens CH27	325	45	3.4	1859	21	AAH81052	Human secreted pro
253	45	3.4	938	19	AAV27142	Novel haemopoietin	326	45	3.4	1877	21	AAZ99797	CDNA encoding a G-
254	45	3.4	938	21	AA446793	DNA encoding a mur	327	45	3.4	2035	8	AAV70687	DNA encoding human
255	45	3.4	938	22	AA041194	Murine haemopoieti	328	45	3.4	2059	24	AAZ38816	Human PSNA CDNA, P
256	45	3.4	941	4	AAV30062	Sequence of a modi	329	45	3.4	2108	21	AAV96570	A core 2 beta-1,6-
257	45	3.4	957	11	AAQ04441	Aequorin gene, Ae	330	45	3.4	2142	22	AAH31355	Human secreted pro
258	45	3.4	958	21	AACT8018	Human cancer assoc	331	45	3.4	2143	23	ABV24475	Human prostate exp
259	45	3.4	958	22	AAH33258	Human colon cancer	332	45	3.4	2143	23	ABV24620	Human prostate exp
260	45	3.4	958	22	AAV32233	Apoaequorin-encodi	333	45	3.4	2143	23	ABV24928	Human prostate exp
261	45	3.4	958	24	ABQ79813	Apoaequorin-encodi	334	45	3.4	2150	22	AAH81781	Human differential
262	45	3.4	958	24	ABQ79826	Apoaequorin-encodi	335	45	3.4	2198	21	AAZ23424	CDNA encoding huma
263	45	3.4	958	24	AAV221188	Aequorea victoria	336	45	3.4	2260	22	AAI97914	Human neuroblastom
264	45	3.4	959	9	AAH81534	PAQ440 aequorin ge	337	45	3.4	2260	22	AAI98068	Human neuroblastom
265	45	3.4	1018	25	ABX78394	Wheat stress respo	338	45	3.4	2326	22	AAH43381	CDNA sequence enco
266	45	3.4	1021	24	ABK66007	Rainbow trout CDNA	339	45	3.4	2381	21	AAV18106	Lung cancer associ
267	45	3.4	1041	21	AAV16005	Human prostate can	340	45	3.4	2602	19	AAAI2416	CDNA encoding a hu
268	45	3.4	1054	25	ACC00688	Glycine max oil tr	341	45	3.4	2836	19	AAV40744	C. felis esterase,
269	45	3.4	1063	22	AAH33256	DNA encoding human	342	45	3.4	2836	19	AAV40745	C. felis esterase,
270	45	3.4	1077	22	AAV27462	CDNA encoding nove	343	45	3.4	2836	19	AAV40745	Ctenocephalides fe
271	45	3.4	1091	22	AAV89723	Maize ZmGn1-1 gl	344	45	3.4	2887	21	AAV56703	Human transitional
272	45	3.4	1091	25	ABX95035	CDNA encoding maiz	345	45	3.4	3084	22	AAV52910	Human CDNA encodin
273	45	3.4	1093	21	AACT7825	Human cancer assoc	346	45	3.4	3084	25	ABX73251	Human novel polynu
274	45	3.4	1093	24	ABK50888	CDNA encoding mur	347	45	3.4	3288	22	AAV05613	Human secreted pro
275	45	3.4	1095	21	AACT7435	Human ORFX ORF2990	348	45	3.4	3288	22	AAV05613	Human secretin-lik
276	45	3.4	1119	22	AAV90638	Human TANGO 369 cD	349	45	3.4	3393	22	AAV90612	Human secreted pro
277	45	3.4	1129	24	ABL90679	Human polynucleoti	350	45	3.4	3393	22	AAV05582	Human secreted pro
278	45	3.4	1143	19	AAV59619	Human secreted pro	351	45	3.4	3393	24	ABV52738	DNA encoding human
279	45	3.4	1143	24	ABV73606	Human CDNA #1 for	352	45	3.4	3397	21	AAV78020	Human cancer assoc
280	45	3.4	1159	22	AAV02547	Human secreted pro	353	45	3.4	3397	22	AAV32711	Human secreted pro
281	45	3.4	1178	24	ABV72167	Nucleotide sequenc	354	45	3.4	3465	20	AAH89616	Human CDNA encodin
282	45	3.4	1186	24	ABK35838	CDNA sequence #229	355	45	3.4	3465	24	AAV59247	Human polynucleoti
283	45	3.4	1212	20	AAV76499	Human WISP-3 prote	356	45	3.4	3465	24	ABA90916	Human secreted pro
284	45	3.4	1212	20	AAV76499	Human WISP-3 prote	357	45	3.4	3477	22	AAV45120	Murine coding sequ
285	45	3.4	1233	21	AAV21869	Human breast and o	358	45	3.4	4115	22	AAH19489	Murine coding sequ
286	45	3.4	1240	24	ABL01589	Human secreted pro	359	45	3.4	4115	22	AAH19493	Murine GABA-B rece
287	45	3.4	1263	24	ABV74466	Maize peroxidase g	360	45	3.4	4365	24	ABA93497	Nucleotide sequenc
288	45	3.4	1266	21	AACT6083	Human ORFX ORF1638	361	45	3.4	4365	25	ABZ68445	Human cell growth,
289	45	3.4	1267	21	AACT7794	Human cancer assoc	362	45	3.4	4524	25	ABV224701	M. sexta acetylcho
290	45	3.4	1280	21	AACT4295	Human secreted pro	363	45	3.4	5554	25	ABV73333	Chemically treated
291	45	3.4	1293	24	AAV63048	Cell death protect	364	45	3.4	6157	24	ABL70182	Signal transductio
292	45	3.4	1300	24	ABK34865	Human CDNA encodin	365	45	3.4	6157	24	ABK31225	Murine coding sequ
293	45	3.4	1303	22	AAV29144	CDNA encoding for	366	45	3.4	7034	22	AAH19496	Human immune syste
294	45	3.4	1303	24	ABV68284	CDNA encoding huma	367	45	3.4	7536	21	ABL33464	Human ORFX ORF2028
295	45	3.4	1307	25	ABZ34881	Coding sequence SE	368	45	3.4	8458	21	AACT6473	Human genomic DNA
296	45	3.4	1315	24	ABZ83451	Mouse MP-1 encodin	369	45	3.4	8711	22	AAV26809	Human novel polynu
297	45	3.4	1340	25	ABV76267	Human GENSET CDNA	370	45	3.4	8711	25	ABV74158	Human novel polynu
298	45	3.4	1405	25	ABX13973	Human Ras-like pro	371	45	3.4	50	50	ABQ77278	Oligo at primer.
299	45	3.4	1414	22	AAH35016	Human colon cancer	372	45	3.4	69	69	AAV88081	3' portion of CDNA
300	45	3.4	1436	22	AAV26093	Human CDNA encodin	373	45	3.4	69	69	AAV02148	Human secreted pro

374	44	3.3	71	25	ABX50202	Bovine EST associa	447	44	3.3	158	22	AAK89971	Human digestive sy
375	44	3.3	77	22	AAK29173	Genomic sequence #	448	44	3.3	158	22	AAK23328	Human prostate can
376	44	3.3	77	22	AAK78766	Human immune/haema	449	44	3.3	158	23	ABL97910	Human testicular a
377	44	3.3	77	22	AAK79578	Human immune/haema	450	44	3.3	158	23	ABL97910	Human testicular a
378	44	3.3	77	22	AAK84669	Human immune/haema	451	44	3.3	158	24	ABS68299	Human DNA-binding
379	44	3.3	77	22	AAK84669	Human immune/haema	452	44	3.3	158	24	ABS68306	Human DNA-binding
380	44	3.3	77	22	ABS68313	Human DNA-binding	453	44	3.3	158	24	ABS68317	Human DNA-binding
381	44	3.3	77	25	ABZ74612	Secreted protein g	454	44	3.3	158	24	ABS68317	Human DNA-binding
382	44	3.3	77	25	ABZ68133	Human secreted pro	455	44	3.3	158	24	ABS68369	Human DNA-binding
383	44	3.3	79	19	AAV32414	Homo sapiens clone	456	44	3.3	158	25	ABZ74608	Secreted protein g
384	44	3.3	79	19	AAV26706	Human novel secret	457	44	3.3	158	25	ABZ68129	Human secreted pro
385	44	3.3	79	22	AAK98430	Human cDNA clone B	458	44	3.3	159	22	AAK56708	Human immune/haema
386	44	3.3	80	19	AAV37197	Oligonucleotide se	459	44	3.3	160	24	ABQ94618	Tumour suppression
387	44	3.3	81	21	AAK13249	Human secreted pro	460	44	3.3	160	24	ABQ94618	Tumour suppression
388	44	3.3	84	24	ABQ94859	Tumour secreted pro	461	44	3.3	160	24	ABQ94618	Tumour suppression
389	44	3.3	85	19	AAV05720	Nucleotide sequenc	462	44	3.3	162	24	ABQ94618	Tumour suppression
390	44	3.3	86	12	AAQ11760	Self-complementary	463	44	3.3	165	24	ABQ94618	Tumour suppression
391	44	3.3	86	22	AAK23317	Human prostate can	464	44	3.3	165	24	ABQ94618	Tumour suppression
392	44	3.3	89	21	AAK78380	Human cancer assoc	465	44	3.3	166	24	ABQ94618	Tumour suppression
393	44	3.3	89	22	AAK23322	Human prostate can	466	44	3.3	166	24	ABQ94618	Tumour suppression
394	44	3.3	89	24	AAK54904	Human colon cancer	467	44	3.3	166	24	ABQ94618	Tumour suppression
395	44	3.3	90	12	AAQ11762	Self-complementary	468	44	3.3	166	24	ABQ94618	Tumour suppression
396	44	3.3	90	21	AAK18395	Lung cancer associ	469	44	3.3	166	24	ABQ94618	Tumour suppression
397	44	3.3	93	25	AAK55117	Bovine EST associa	470	44	3.3	166	24	ABQ94618	Tumour suppression
398	44	3.3	95	25	AAK43810	Bovine EST associa	471	44	3.3	166	24	ABQ94618	Tumour suppression
399	44	3.3	98	20	AAK00174	Porcine reproducti	472	44	3.3	166	24	ABQ94618	Tumour suppression
400	44	3.3	98	18	AAK91300	Human M97-2 secret	473	44	3.3	166	24	ABQ94618	Tumour suppression
401	44	3.3	101	18	AAV00420	3' fragment of clo	474	44	3.3	166	24	ABQ94618	Tumour suppression
402	44	3.3	103	25	AAK61529	Arabidopsis thalia	475	44	3.3	166	24	ABQ94618	Tumour suppression
403	44	3.3	109	23	ABK41815	cDNA encoding nove	476	44	3.3	166	24	ABQ94618	Tumour suppression
404	44	3.3	113	25	ABK54764	Bovine EST associa	477	44	3.3	166	24	ABQ94618	Tumour suppression
405	44	3.3	114	25	ABK61401	Arabidopsis thalia	478	44	3.3	166	24	ABQ94618	Tumour suppression
406	44	3.3	115	25	ABK60912	Arabidopsis thalia	479	44	3.3	166	24	ABQ94618	Tumour suppression
407	44	3.3	116	24	AAK63020	Cell death protect	480	44	3.3	166	24	ABQ94618	Tumour suppression
408	44	3.3	118	25	AAK43819	Bovine EST associa	481	44	3.3	166	24	ABQ94618	Tumour suppression
409	44	3.3	120	16	AAQ52429	Human subtelomeric	482	44	3.3	166	24	ABQ94618	Tumour suppression
410	44	3.3	120	16	AAQ57011	Subtelomeric cDNA	483	44	3.3	166	24	ABQ94618	Tumour suppression
411	44	3.3	120	19	AAK96338	Subtelomeric cDNA	484	44	3.3	166	24	ABQ94618	Tumour suppression
412	44	3.3	120	25	ABK50021	Telomere length an	485	44	3.3	166	24	ABQ94618	Tumour suppression
413	44	3.3	125	24	ABQ94578	Tumour suppression	486	44	3.3	166	24	ABQ94618	Tumour suppression
414	44	3.3	130	22	AAK56565	Human cDNA for an	487	44	3.3	166	24	ABQ94618	Tumour suppression
415	44	3.3	130	25	ABK42765	Bovine EST associa	488	44	3.3	166	24	ABQ94618	Tumour suppression
416	44	3.3	137	25	ABK40521	Bovine EST associa	489	44	3.3	166	24	ABQ94618	Tumour suppression
417	44	3.3	138	25	ABK50278	Bovine EST associa	490	44	3.3	166	24	ABQ94618	Tumour suppression
418	44	3.3	140	18	AAK76781	Staphylococcus aur	491	44	3.3	166	24	ABQ94618	Tumour suppression
419	44	3.3	141	16	AAK06012	Immunodominant fra	492	44	3.3	166	24	ABQ94618	Tumour suppression
420	44	3.3	144	19	AAV21239	Homo sapiens clone	493	44	3.3	166	24	ABQ94618	Tumour suppression
421	44	3.3	144	20	AAK77331	Human secreted pro	494	44	3.3	166	24	ABQ94618	Tumour suppression
422	44	3.3	145	24	ABK49455	Sequence #57 used	495	44	3.3	166	24	ABQ94618	Tumour suppression
423	44	3.3	145	24	ABK30642	Plant dwarfing/stu	496	44	3.3	166	24	ABQ94618	Tumour suppression
424	44	3.3	147	24	ABV96469	Human pancreatic c	497	44	3.3	166	24	ABQ94618	Tumour suppression
425	44	3.3	152	22	AAK16268	Human breast or ov	498	44	3.3	166	24	ABQ94618	Tumour suppression
426	44	3.3	152	22	AAK09029	Human DNA-binding	499	44	3.3	166	24	ABQ94618	Tumour suppression
427	44	3.3	152	22	AAK09029	Human breast cance	500	44	3.3	166	24	ABQ94618	Tumour suppression
428	44	3.3	152	22	AAK16670	Human pancreatic r	501	44	3.3	166	24	ABQ94618	Tumour suppression
429	44	3.3	152	22	AAK29169	Genomic sequence #	502	44	3.3	166	24	ABQ94618	Tumour suppression
430	44	3.3	152	22	AAK06722	Human reproductive	503	44	3.3	166	24	ABQ94618	Tumour suppression
431	44	3.3	152	22	AAK89972	Human digestive sy	504	44	3.3	166	24	ABQ94618	Tumour suppression
432	44	3.3	152	22	AAK16268	Human breast or ov	505	44	3.3	166	24	ABQ94618	Tumour suppression
433	44	3.3	152	24	AAK68309	Human DNA-binding	506	44	3.3	166	24	ABQ94618	Tumour suppression
434	44	3.3	153	24	ABL37453	Human colon tumour	507	44	3.3	166	24	ABQ94618	Tumour suppression
435	44	3.3	156	22	AAK60040	Human cancer agent	508	44	3.3	166	24	ABQ94618	Tumour suppression
436	44	3.3	156	22	AAK63711	Human immune/haema	509	44	3.3	166	24	ABQ94618	Tumour suppression
437	44	3.3	157	23	ABV57926	Human prostate exp	510	44	3.3	166	24	ABQ94618	Tumour suppression
438	44	3.3	158	22	AAK35938	Human cardiovascular	511	44	3.3	166	24	ABQ94618	Tumour suppression
439	44	3.3	158	22	AAK16669	Human cardiac r	512	44	3.3	166	24	ABQ94618	Tumour suppression
440	44	3.3	158	22	AAK29159	Genomic sequence #	513	44	3.3	166	24	ABQ94618	Tumour suppression
441	44	3.3	158	22	AAK29166	Genomic sequence #	514	44	3.3	166	24	ABQ94618	Tumour suppression
442	44	3.3	158	22	AAK29177	Genomic sequence #	515	44	3.3	166	24	ABQ94618	Tumour suppression
443	44	3.3	158	22	AAK29229	Human reproductive	516	44	3.3	166	24	ABQ94618	Tumour suppression
444	44	3.3	158	22	AAK04802	Human reproductive	517	44	3.3	166	24	ABQ94618	Tumour suppression
445	44	3.3	158	22	AAK05017	Human immune/haema	518	44	3.3	166	24	ABQ94618	Tumour suppression
446	44	3.3	158	22	AAK73939	Human immune/haema	519	44	3.3	166	24	ABQ94618	Tumour suppression
447	44	3.3	158	22	AAK78756	Human immune/haema	520	44	3.3	166	24	ABQ94618	Tumour suppression
448	44	3.3	158	22	AAK46665	Human immune/haema	521	44	3.3	166	24	ABQ94618	Tumour suppression
449	44	3.3	158	22	AAK46665	Human immune/haema	522	44	3.3	166	24	ABQ94618	Tumour suppression
450	44	3.3	158	22	AAK46665	Human immune/haema	523	44	3.3	166	24	ABQ94618	Tumour suppression
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452	44	3.3	158	22	AAK46665	Human immune/haema	525	44	3.3	166	24	ABQ94618	Tumour suppression
453	44	3.3	158	22	AAK46665	Human immune/haema	526	44	3.3	166	24	ABQ94618	Tumour suppression
454	44	3.3	158	22	AAK46665	Human immune/haema	527	44	3.3	166	24	ABQ94618	Tumour suppression
455	44	3.3	158	22	AAK46665	Human immune/haema	528	44	3.3	166	24	ABQ94618	Tumour suppression
456	44	3.3	158	22	AAK46665	Human immune/haema	529	44	3.3	166	24	ABQ94618	Tumour suppression
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458	44	3.3	158	22	AAK46665	Human immune/haema	531	44	3.3	166	24	ABQ94618	Tumour suppression
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460	44	3.3	158	22	AAK46665	Human immune/haema	533	44	3.3	166	24	ABQ94618	Tumour suppression
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462	44	3.3	158	22	AAK46665	Human immune/haema	535	44	3.3	166	24	ABQ94618	Tumour suppression
463	44	3.3	158	22	AAK46665	Human immune/haema	536	44	3.3	166	24	ABQ94618	Tumour suppression
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468	44	3.3	158	22	AAK46665	Human immune/haema	541	44	3.3	166	24	ABQ94618	Tumour suppression
469	44	3.3	158	22	AAK46665	Human immune/haema	542	44	3.3	166	24	ABQ94618	Tumour suppression
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471	44	3.3	158	22	AAK46665	Human immune/haema	544	44	3.3	166	24	ABQ94618	Tumour suppression
472	44	3.3	158	22	AAK46665	Human immune/haema	545	44	3.3	166	24	ABQ94618	Tumour suppression
473	44	3.3	158	22	AAK46665	Human immune/haema	546	44	3.3	166	24	ABQ94618	Tumour suppression
474	44												

C 520	44	3.3	220	25	ABX49357	Bovine EST associa	593	44	3.3	267	23	ABV56597	Human prostate exp
521	44	3.3	221	23	ABV19669	Human prostate exp	C 594	44	3.3	268	23	ABV38724	Human prostate exp
522	44	3.3	222	14	AAQ46071	Sequence downstre	C 595	44	3.3	269	23	ABV07492	Human prostate exp
523	44	3.3	222	22	AAQ86777	Downstream sequenc	C 596	44	3.3	271	22	AAL16362	Human breast canc
C 524	44	3.3	222	24	ABZ08197	Human leukocyte de	C 597	44	3.3	272	22	ABA12564	Human nervous syst
525	44	3.3	223	23	ABV55382	Human prostate exp	C 598	44	3.3	272	22	AAL12612	Human breast canc
526	44	3.3	223	24	ABG68859	Human RecQ protein	C 599	44	3.3	272	25	ABX41821	Bovine EST associa
C 527	44	3.3	223	25	ABX35502	Bovine EST associa	C 600	44	3.3	273	23	ABV56926	Human prostate exp
528	44	3.3	226	22	AAS29055	CDNA encoding for	C 601	44	3.3	273	24	ABQ54673	Human ovarian anti
C 529	44	3.3	226	22	AAH69412	Human cervical can	C 602	44	3.3	274	23	ABV58263	Human prostate exp
C 530	44	3.3	226	23	ABV05927	Human prostate exp	C 603	44	3.3	274	24	ABZ08581	Human leukocyte de
531	44	3.3	226	23	ABV19006	Human prostate exp	C 604	44	3.3	276	23	ABV58412	Human prostate exp
C 532	44	3.3	226	24	ABZ08680	Human leukocyte de	C 605	44	3.3	276	25	ABX44966	Bovine EST associa
533	44	3.3	226	24	ABG68195	CDNA encoding huma	C 606	44	3.3	277	23	ABV57365	Human prostate exp
C 534	44	3.3	228	25	ABX45169	Bovine EST associa	C 607	44	3.3	277	25	ABX37131	Bovine EST associa
535	44	3.3	228	25	AAF68277	Human lung tumour	C 608	44	3.3	277	25	ABX47508	Bovine EST associa
536	44	3.3	229	23	ABV57008	Human prostate exp	C 609	44	3.3	278	22	AAH69999	Human cervical can
537	44	3.3	229	23	ABV57683	Human prostate exp	C 610	44	3.3	279	23	ABV55135	Human prostate exp
538	44	3.3	229	24	ABX38188	CDNA encoding clon	C 611	44	3.3	280	23	ABV58623	Human prostate exp
539	44	3.3	229	25	ACA10517	Lung cancer therap	C 612	44	3.3	281	21	AAQ00286	Human colon cancer
540	44	3.3	229	25	ABX99468	Human prostate exp	C 613	44	3.3	281	23	ABV35976	Human prostate exp
541	44	3.3	230	22	AAH33118	Human colon cancer	C 614	44	3.3	282	23	ABV47775	Human prostate exp
542	44	3.3	230	22	ABV57305	Human prostate exp	C 615	44	3.3	282	23	ABV61303	Human prostate exp
543	44	3.3	230	23	ABV57465	Human prostate exp	C 616	44	3.3	285	22	AAL34854	Human musculoskele
544	44	3.3	230	23	ABV58314	Human prostate exp	C 617	44	3.3	285	23	ABV18565	Human prostate exp
545	44	3.3	230	25	ABX45059	Bovine EST associa	C 618	44	3.3	285	25	ABX57842	CDNA encoding nove
546	44	3.3	232	22	AAH33358	Human colon cancer	C 619	44	3.3	286	25	ABX48177	Bovine EST associa
547	44	3.3	232	23	ABV58523	Human prostate exp	C 620	44	3.3	287	24	ABL87079	Human ovarian can
548	44	3.3	233	23	AAH33064	CDNA encoding for	C 621	44	3.3	287	25	ABT22943	Breast cancer mark
549	44	3.3	233	22	AAH33064	Human colon cancer	C 622	44	3.3	287	25	ABX40723	Bovine EST associa
550	44	3.3	233	24	ABG68269	CDNA encoding huma	C 623	44	3.3	289	14	AAQ53450	Sequence of the 3'
551	44	3.3	234	23	ABV57891	Human prostate exp	C 624	44	3.3	289	22	AAL16073	Human breast canc
C 552	44	3.3	235	23	ABV60929	Human prostate exp	C 625	44	3.3	289	22	AAI8427	Human polynucleoti
553	44	3.3	236	23	ABV56953	Human prostate exp	C 626	44	3.3	289	23	ABV49828	Human prostate exp
C 554	44	3.3	236	25	ABT22889	Breast cancer mark	C 627	44	3.3	291	20	AAZ13376	Human gene express
C 555	44	3.3	237	23	ABV07534	Human prostate exp	C 628	44	3.3	291	23	ABV56619	Human prostate exp
C 556	44	3.3	237	25	ABX49378	Bovine EST associa	C 629	44	3.3	291	24	ABK44641	CDNA encoding colo
C 557	44	3.3	238	22	ABG60314	Human cancer agent	C 630	44	3.3	291	25	ABX36078	Bovine EST associa
558	44	3.3	239	23	ABV11191	Human nervous syst	C 631	44	3.3	291	25	ABX48529	Bovine EST associa
C 559	44	3.3	239	23	ABV56818	Human prostate exp	C 632	44	3.3	292	19	AAV21153	3' nucleotide port
C 560	44	3.3	239	25	ABX46273	Bovine EST associa	C 633	44	3.3	292	19	AAV21153	3' nucleotide port
C 561	44	3.3	239	25	ABX48174	Bovine EST associa	C 634	44	3.3	293	22	AAV49135	Human prostate exp
C 562	44	3.3	240	18	AAH76782	Staphylococcus aur	C 635	44	3.3	293	22	AAL25205	Human breast canc
563	44	3.3	240	23	ABV58851	Human prostate exp	C 636	44	3.3	294	22	AAK97279	Human cDNA 3'-end
C 564	44	3.3	241	23	ABV61751	Human prostate exp	C 637	44	3.3	294	22	ABV56381	Human prostate exp
C 565	44	3.3	241	25	ABX40612	Bovine EST associa	C 638	44	3.3	294	25	ABZ54909	Aspergillus oryzae
C 566	44	3.3	241	25	ABX42739	Bovine EST associa	C 639	44	3.3	295	22	AAS29052	CDNA encoding for
C 567	44	3.3	241	25	ABX47809	Bovine EST associa	C 640	44	3.3	295	23	ABV19977	Human prostate exp
C 568	44	3.3	242	22	AAL25805	Human breast canc	C 641	44	3.3	295	24	ABS68192	CDNA encoding huma
C 569	44	3.3	242	25	ABX38052	Bovine EST associa	C 642	44	3.3	296	22	AAL16259	Human breast canc
570	44	3.3	243	23	ABV56639	Human prostate exp	C 643	44	3.3	296	22	AAL21959	Human breast canc
C 571	44	3.3	245	22	AAL25909	Human breast canc	C 644	44	3.3	299	22	ABL87398	Human ovarian can
C 572	44	3.3	247	22	AAH71353	Human cervical can	C 645	44	3.3	300	22	AAH70049	Human ovarian can
573	44	3.3	247	23	ABV19174	Human prostate exp	C 646	44	3.3	300	25	ABX41086	Bovine EST associa
C 574	44	3.3	248	23	ABV60876	Human prostate exp	C 647	44	3.3	303	23	ABV19295	Human prostate exp
C 575	44	3.3	250	23	ABV59115	Human prostate exp	C 648	44	3.3	303	23	ABV49738	Human prostate exp
C 576	44	3.3	252	23	ABV13586	Human prostate exp	C 649	44	3.3	304	22	AAV29128	CDNA encoding for
C 577	44	3.3	252	22	AAH82206	Rat differential t	C 650	44	3.3	304	23	ABV19428	Human prostate exp
C 578	44	3.3	256	23	ABV52378	Human prostate exp	C 651	44	3.3	304	23	ABV55655	Human prostate exp
C 579	44	3.3	256	25	ABX44248	Bovine EST associa	C 652	44	3.3	305	24	ABV58043	CDNA encoding huma
580	44	3.3	257	23	ABV49122	Human prostate exp	C 653	44	3.3	306	24	ABZ08725	Human leukocyte de
581	44	3.3	257	23	ABV59128	Human prostate exp	C 654	44	3.3	307	22	ABZ29073	CDNA encoding for
C 582	44	3.3	257	25	ABX43725	Bovine EST associa	C 655	44	3.3	307	23	ABV48143	Human prostate exp
C 583	44	3.3	258	22	AAL19074	Human breast canc	C 656	44	3.3	307	24	ABG68213	CDNA encoding huma
584	44	3.3	258	23	ABV56911	Human prostate exp	C 657	44	3.3	308	25	ABX42505	Bovine EST associa
C 585	44	3.3	259	25	ABX38288	Bovine EST associa	C 658	44	3.3	309	23	ABV44994	Human prostate exp
C 586	44	3.3	259	25	ABX42088	Bovine EST associa	C 659	44	3.3	309	23	ABV49356	Human prostate exp
587	44	3.3	262	24	ABX55426	Human colon cancer	C 660	44	3.3	309	23	ABV57373	Human prostate exp
C 588	44	3.3	264	24	ABL87207	Human ovarian can	C 661	44	3.3	310	22	ABH71505	Human cervical can
C 589	44	3.3	265	22	AAH71554	Human cervical can	C 662	44	3.3	310	22	ABL87211	Human ovarian can
C 590	44	3.3	266	22	AAL13089	Human breast canc	C 663	44	3.3	311	23	ABV48785	Human prostate exp
C 591	44	3.3	266	23	ABV07596	Human prostate exp	C 664	44	3.3	311	24	ABL87180	Human ovarian can
592	44	3.3	267	22	AAS60607	Human cancer agent	C 665	44	3.3	312	25	ABX41150	Bovine EST associa

666	44	3.3	312	25	ABX43249	Bovine EST associa	C 739	44	3.3	352	23	ABV60857	Human prostate exp
667	44	3.3	313	25	ABX37505	Bovine EST associa	740	44	3.3	353	22	AAI80163	Human polynucleoti
668	44	3.3	314	22	AAQ29145	CDNA encoding for	741	44	3.3	354	22	AAI87541	Human polynucleoti
669	44	3.3	314	22	AAK61200	Human immune/haema	742	44	3.3	355	22	AAI81491	Human polynucleoti
670	44	3.3	314	23	ABV04305	Human prostate exp	C 743	44	3.3	355	25	ABX37780	Bovine EST associa
671	44	3.3	314	23	ABV58492	Human prostate exp	C 744	44	3.3	355	25	ABX49592	Bovine EST associa
672	44	3.3	314	24	ABV58492	CDNA encoding huma	745	44	3.3	356	23	ABV43201	Human prostate exp
673	44	3.3	315	22	AAH71521	Human cervical can	746	44	3.3	357	22	AAI87170	Human polynucleoti
674	44	3.3	315	22	ABV54312	Human prostate exp	747	44	3.3	358	23	ABV48348	Human prostate exp
675	44	3.3	317	23	ABV15175	Human prostate exp	748	44	3.3	359	23	ABV18767	Human prostate exp
676	44	3.3	317	23	ABV58763	Human prostate exp	749	44	3.3	359	23	ABV56960	Human prostate exp
677	44	3.3	317	25	ABX37534	Bovine EST associa	C 750	44	3.3	359	24	ABQ85688	Arabidopsis thalia
678	44	3.3	318	23	ABV56059	Human prostate exp	C 751	44	3.3	360	22	AAI20475	Human breast cance
679	44	3.3	318	24	ABT10735	Human breast cance	752	44	3.3	360	23	ABV59054	Human prostate exp
680	44	3.3	320	22	ABV55020	Bovine EST associa	C 753	44	3.3	360	24	ABQ85662	Arabidopsis thalia
681	44	3.3	320	22	AAI84550	Human polynucleoti	754	44	3.3	361	22	AAI87168	Human polynucleoti
682	44	3.3	320	22	ABV49069	Human prostate exp	755	44	3.3	361	22	AAI88713	Human polynucleoti
683	44	3.3	320	22	AAI08164	Human breast cance	756	44	3.3	361	23	ABV56706	Human prostate exp
684	44	3.3	321	23	ABV34590	Human prostate exp	C 757	44	3.3	361	24	ABL85588	Human ovarian canc
685	44	3.3	321	23	ABV43446	Human prostate exp	758	44	3.3	362	22	AAI83208	Human polynucleoti
686	44	3.3	322	22	AAI19416	Human breast cance	C 759	44	3.3	362	25	ABX40225	Bovine EST associa
687	44	3.3	323	23	ABV60996	Human prostate exp	C 760	44	3.3	363	23	ABV12992	Human prostate exp
688	44	3.3	323	25	ABX44970	Bovine EST associa	761	44	3.3	364	22	AAH34350	Human colon cancer
689	44	3.3	324	23	ABV57099	Human prostate exp	762	44	3.3	364	23	ABV56939	Human prostate exp
690	44	3.3	325	22	AAQ29049	CDNA encoding for	763	44	3.3	364	25	ABX44254	Bovine EST associa
691	44	3.3	325	24	ABQ68189	Bovine EST associa	764	44	3.3	365	22	AAI83450	Human polynucleoti
692	44	3.3	325	25	ABX43454	Human polynucleoti	765	44	3.3	365	22	AAI86853	Human polynucleoti
693	44	3.3	326	22	AAI90437	Human polynucleoti	766	44	3.3	365	22	AAI87543	Human polynucleoti
694	44	3.3	327	23	ABV55213	Human prostate exp	767	44	3.3	365	22	AAI88393	Human polynucleoti
695	44	3.3	331	23	ABV49436	Human prostate exp	768	44	3.3	366	21	AAAC98273	Human colon cancer
696	44	3.3	331	23	ABV56426	Human prostate exp	769	44	3.3	366	22	AAI82117	Human polynucleoti
697	44	3.3	331	25	AAH22555	Breast cancer mark	770	44	3.3	366	22	AAI87537	Human polynucleoti
698	44	3.3	332	22	AAH71330	Human cervical can	771	44	3.3	367	23	ABV19488	Human prostate exp
699	44	3.3	332	23	ABV13891	Human prostate exp	772	44	3.3	367	23	ABV54973	Human prostate exp
700	44	3.3	332	23	ABV49368	Human prostate exp	C 773	44	3.3	368	22	AAQ60046	Human cancer agent
701	44	3.3	332	23	ABV55846	Human prostate exp	774	44	3.3	368	22	AAI90378	Human polynucleoti
702	44	3.3	332	23	ABV56463	Human cancer agent	775	44	3.3	370	21	AAZ51574	Haematobia irritan
703	44	3.3	335	22	AAQ60452	Human prostate exp	776	44	3.3	370	22	AAI88518	Human polynucleoti
704	44	3.3	335	22	AAI19579	Human breast cance	777	44	3.3	370	22	AAK56906	Human immune/haema
705	44	3.3	335	22	AAI84803	Human polynucleoti	778	44	3.3	370	22	ABX41004	Bovine EST associa
706	44	3.3	337	23	ABV55706	Human prostate exp	779	44	3.3	372	9	AAH80489	Cowpea trypsin inh
707	44	3.3	337	23	ABV58905	Human prostate exp	780	44	3.3	372	22	AAI89007	Human polynucleoti
708	44	3.3	337	24	ABQ66019	Arabidopsis thalia	781	44	3.3	372	22	AAI91018	Human polynucleoti
709	44	3.3	337	25	ABX41811	Bovine EST associa	C 782	44	3.3	372	23	ABV37528	Human prostate exp
710	44	3.3	338	22	AAI80023	Human polynucleoti	C 783	44	3.3	373	25	ABX35671	Bovine EST associa
711	44	3.3	338	23	ABV48996	Human prostate exp	784	44	3.3	373	25	ABX38490	Bovine EST associa
712	44	3.3	338	23	ABV60873	Human prostate exp	C 785	44	3.3	374	22	AAI84577	Human polynucleoti
713	44	3.3	338	24	ABZ08610	Human leukocyte de	786	44	3.3	374	22	AAI84793	Human polynucleoti
714	44	3.3	339	23	ABV56910	Human prostate exp	787	44	3.3	374	22	AAI91055	Human polynucleoti
715	44	3.3	340	20	AAV89136	EST clone BR309	788	44	3.3	375	18	AAH84939	Human prostate pro
716	44	3.3	341	22	AAI83390	Human polynucleoti	789	44	3.3	375	20	AAK35869	CDNA encoding a pr
717	44	3.3	341	23	ABV49421	Human prostate exp	790	44	3.3	375	22	AAI90861	Human polynucleoti
718	44	3.3	343	22	AAI88988	Human polynucleoti	C 791	44	3.3	375	23	ABV44911	Human prostate exp
719	44	3.3	343	23	ABV60943	Human prostate exp	792	44	3.3	375	23	ABV58452	Human prostate exp
720	44	3.3	344	22	AAI85033	Human polynucleoti	C 793	44	3.3	375	25	ABX49849	Bovine EST associa
721	44	3.3	344	25	ABX47837	Bovine EST associa	794	44	3.3	376	22	AAI84760	Human polynucleoti
722	44	3.3	345	23	ABV07703	Human prostate exp	795	44	3.3	376	22	AAI87530	Human polynucleoti
723	44	3.3	345	23	AAV60689	Human prostate exp	796	44	3.3	376	23	ABV57109	Human prostate exp
724	44	3.3	346	22	AAI87483	Human polynucleoti	797	44	3.3	377	25	ABX44260	Bovine EST associa
725	44	3.3	346	22	AAI93468	Human polynucleoti	798	44	3.3	378	22	AAI82660	Human polynucleoti
726	44	3.3	347	22	AAI83215	Human polynucleoti	799	44	3.3	378	22	AAI83210	Human polynucleoti
727	44	3.3	347	22	AAI87559	Human polynucleoti	800	44	3.3	378	22	AAI90863	Human polynucleoti
728	44	3.3	347	25	ABX35931	Bovine EST associa	C 801	44	3.3	378	22	AAI90863	Sugarcane plant ge
729	44	3.3	347	25	ABX38206	Bovine EST associa	C 802	44	3.3	379	22	AAI20476	Human breast cance
730	44	3.3	349	24	ABQ85842	Arabidopsis thalia	803	44	3.3	380	22	AAI188350	Human polynucleoti
731	44	3.3	350	22	AAI82669	Human polynucleoti	804	44	3.3	380	22	AAK91627	Human CDNA 5'-end
732	44	3.3	350	24	ABQ85831	Arabidopsis thalia	805	44	3.3	380	22	AAK93551	Human cDNA clone r
733	44	3.3	350	24	ABQ54299	Human ovarian anti	806	44	3.3	380	23	ABV49790	Human prostate exp
734	44	3.3	350	25	ABX46565	Bovine EST associa	C 807	44	3.3	381	22	AAI86023	Human polynucleoti
735	44	3.3	351	22	AAI82851	Human polynucleoti	C 808	44	3.3	381	23	ABV14968	Human prostate exp
736	44	3.3	351	23	ABV55243	Human prostate exp	809	44	3.3	382	22	AAI82890	Human polynucleoti
737	44	3.3	351	24	ABQ85821	Arabidopsis thalia	810	44	3.3	382	22	AAI84706	Human polynucleoti
738	44	3.3	352	23	ABV56898	Human prostate exp	811	44	3.3	382	22	AAI87526	Human polynucleoti

812	44	3.3	382	22	AA187806	Human polynucleoti	C 885	44	3.3	396	24	ABL48777	Ovarian carcinoma
813	44	3.3	382	22	AA187942	Human polynucleoti	C 886	44	3.3	396	24	ABL48801	Ovarian carcinoma
814	44	3.3	382	22	ABV42927	Human prostate exp	C 887	44	3.3	396	24	ABL48812	Ovarian carcinoma
815	44	3.3	382	23	ABV49016	Human prostate exp	C 888	44	3.3	397	22	AA180153	Human polynucleoti
816	44	3.3	382	23	ABV54300	Human prostate exp	C 889	44	3.3	397	22	AA182664	Human polynucleoti
817	44	3.3	382	23	ABV56122	Human prostate exp	C 890	44	3.3	397	25	ABX48619	Bovine EST associa
818	44	3.3	382	23	AA188525	Human polynucleoti	C 891	44	3.3	398	22	AA188050	Human polynucleoti
819	44	3.3	383	22	AA188525	Human polynucleoti	C 892	44	3.3	398	22	AA188703	Human polynucleoti
820	44	3.3	383	22	AA188530	Human prostate exp	C 893	44	3.3	398	23	ABV34113	Human prostate exp
821	44	3.3	383	23	ABV34060	Human prostate exp	C 894	44	3.3	398	23	ABV42975	Human prostate exp
822	44	3.3	383	23	ABV57015	Human secreted pro	C 895	44	3.3	398	23	ABV58301	Human prostate exp
823	44	3.3	383	24	ABV57015	Human secreted pro	C 896	44	3.3	398	25	ABX46765	Bovine EST associa
824	44	3.3	384	21	AA183079	Human polynucleoti	C 897	44	3.3	399	17	AA1830261	Cotton fibre cell-
825	44	3.3	384	22	AA185450	Human polynucleoti	C 898	44	3.3	399	17	AA1830261	Cotton fibre-speci
826	44	3.3	384	22	AA188641	Human polynucleoti	C 899	44	3.3	399	18	AA1830261	Cotton fibre-speci
827	44	3.3	384	22	AA188641	Human polynucleoti	C 900	44	3.3	399	18	AA1830261	Cotton fibre-speci
828	44	3.3	384	22	AA188641	Human polynucleoti	C 901	44	3.3	399	21	AA1830261	Cotton fibre-speci
829	44	3.3	384	22	AA188641	Human polynucleoti	C 902	44	3.3	399	21	AA1830261	Cotton fibre-speci
830	44	3.3	385	22	AA188641	Human polynucleoti	C 903	44	3.3	399	22	AA1830261	Cotton fibre-speci
831	44	3.3	385	25	AA188641	Human polynucleoti	C 904	44	3.3	399	22	AA1830261	Cotton fibre-speci
832	44	3.3	386	22	AA188641	Human polynucleoti	C 905	44	3.3	399	22	AA1830261	Cotton fibre-speci
833	44	3.3	386	22	AA188641	Human polynucleoti	C 906	44	3.3	399	25	ABX62704	Arabidopsis thalia
834	44	3.3	386	22	AA188641	Human polynucleoti	C 907	44	3.3	400	22	AA1830261	Human polynucleoti
835	44	3.3	386	22	AA188641	Human polynucleoti	C 908	44	3.3	400	22	AA1830261	Human polynucleoti
836	44	3.3	386	22	AA188641	Human polynucleoti	C 909	44	3.3	400	22	AA1830261	Human polynucleoti
837	44	3.3	386	24	ABZ08601	Human leukocyte de	C 910	44	3.3	400	22	AA1830261	Human polynucleoti
838	44	3.3	387	22	AA188641	Human breast cancer	C 911	44	3.3	400	22	AA1830261	Human polynucleoti
839	44	3.3	387	22	AA188641	Human breast cancer	C 912	44	3.3	400	22	AA1830261	Human polynucleoti
840	44	3.3	388	22	AA188641	Human polynucleoti	C 913	44	3.3	400	22	AA1830261	Human polynucleoti
841	44	3.3	388	22	AA188641	Human polynucleoti	C 914	44	3.3	400	22	AA1830261	Human polynucleoti
842	44	3.3	388	25	ABX41515	Bovine EST associa	C 915	44	3.3	400	23	ABV54560	Human prostate exp
843	44	3.3	389	22	AA188641	Human breast cancer	C 916	44	3.3	400	23	ABV54560	Human prostate exp
844	44	3.3	389	22	AA188641	Human breast cancer	C 917	44	3.3	401	22	AA1830261	Human polynucleoti
845	44	3.3	389	22	AA188641	Human breast cancer	C 918	44	3.3	401	22	AA1830261	Human polynucleoti
846	44	3.3	389	22	AA188641	Human polynucleoti	C 919	44	3.3	401	25	ABX53255	Bovine EST associa
847	44	3.3	389	22	AA188641	Human polynucleoti	C 920	44	3.3	402	22	AA1830261	Human breast cancer
848	44	3.3	389	22	AA188641	Human polynucleoti	C 921	44	3.3	402	22	AA1830261	Human polynucleoti
849	44	3.3	389	22	AA188641	Human polynucleoti	C 922	44	3.3	402	22	AA1830261	Human polynucleoti
850	44	3.3	389	24	ABX68075	Human polynucleoti	C 923	44	3.3	402	22	AA1830261	Human polynucleoti
851	44	3.3	390	22	AA183046	Human polynucleoti	C 924	44	3.3	402	22	AA1830261	Human polynucleoti
852	44	3.3	390	22	AA183046	Human polynucleoti	C 925	44	3.3	402	24	ABZ08435	Human leukocyte de
853	44	3.3	390	22	AA183046	Human polynucleoti	C 926	44	3.3	402	24	ABZ08435	Human leukocyte de
854	44	3.3	390	22	AA183046	Human polynucleoti	C 927	44	3.3	403	22	AA1830261	Human polynucleoti
855	44	3.3	390	22	AA183046	Human polynucleoti	C 928	44	3.3	403	22	AA1830261	Human polynucleoti
856	44	3.3	391	22	AA183046	Human polynucleoti	C 929	44	3.3	403	22	AA1830261	Human polynucleoti
857	44	3.3	391	22	AA183046	Human polynucleoti	C 930	44	3.3	403	22	AA1830261	Human polynucleoti
858	44	3.3	391	22	AA183046	Human polynucleoti	C 931	44	3.3	403	22	AA1830261	Human polynucleoti
859	44	3.3	392	22	AA183046	Human polynucleoti	C 932	44	3.3	404	22	AA1830261	Human polynucleoti
860	44	3.3	392	22	AA183046	Human polynucleoti	C 933	44	3.3	404	22	AA1830261	Human polynucleoti
861	44	3.3	392	22	AA183046	Human polynucleoti	C 934	44	3.3	404	22	AA1830261	Human polynucleoti
862	44	3.3	392	23	ABV54346	Human prostate exp	C 935	44	3.3	404	22	AA1830261	Human polynucleoti
863	44	3.3	392	25	ABX37469	Bovine EST associa	C 936	44	3.3	404	23	ABV42928	Human prostate exp
864	44	3.3	392	25	ABX37469	Bovine EST associa	C 937	44	3.3	404	25	ABX42928	Human prostate exp
865	44	3.3	393	22	AA187824	Human polynucleoti	C 938	44	3.3	404	25	ABX42928	Human prostate exp
866	44	3.3	393	25	ABX39417	Bovine EST associa	C 939	44	3.3	404	25	ABX39417	Bovine EST associa
867	44	3.3	394	22	AA184810	Human contig polyn	C 940	44	3.3	405	25	ABX45586	Bovine EST associa
868	44	3.3	394	23	ABV18659	Human prostate exp	C 941	44	3.3	405	22	AA1830261	Human polynucleoti
869	44	3.3	394	23	ABV49244	Human prostate exp	C 942	44	3.3	405	22	AA1830261	Human polynucleoti
870	44	3.3	394	23	ABV57207	Human prostate exp	C 943	44	3.3	405	22	AA1830261	Human polynucleoti
871	44	3.3	394	23	ABV57207	Human prostate exp	C 944	44	3.3	405	22	AA1830261	Human polynucleoti
872	44	3.3	394	25	ABX42549	Bovine EST associa	C 945	44	3.3	406	22	AA1830261	Human polynucleoti
873	44	3.3	395	21	AA1830261	Human secreted pro	C 946	44	3.3	406	22	AA1830261	Human polynucleoti
874	44	3.3	395	22	AA1830261	Human polynucleoti	C 947	44	3.3	406	22	AA1830261	Human polynucleoti
875	44	3.3	395	22	AA1830261	Human polynucleoti	C 948	44	3.3	406	23	ABV60840	Human prostate exp
876	44	3.3	395	22	AA1830261	Human polynucleoti	C 949	44	3.3	407	22	AA1830261	Human polynucleoti
877	44	3.3	396	22	AA1830261	Human ovarian carc	C 950	44	3.3	407	22	AA1830261	Human polynucleoti
878	44	3.3	396	22	AA1830261	Human ovarian carc	C 951	44	3.3	407	22	AA1830261	Human polynucleoti
879	44	3.3	396	22	AA1830261	Human ovarian carc	C 952	44	3.3	407	22	AA1830261	Human polynucleoti
880	44	3.3	396	22	AA1830261	Human ovarian carc	C 953	44	3.3	407	23	ABV60716	Human prostate exp
881	44	3.3	396	24	ABT03094	Human ovarian carc	C 954	44	3.3	408	22	AA1830261	Human polynucleoti
882	44	3.3	396	24	ABT03094	Human ovarian carc	C 955	44	3.3	408	22	AA1830261	Human polynucleoti
883	44	3.3	396	24	ABT03094	Human ovarian carc	C 956	44	3.3	408	23	ABV14972	Human prostate exp
884	44	3.3	396	24	ABT03094	Human ovarian carc	C 957	44	3.3	408	25	ABX41098	Bovine EST associa

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958 44 3.3 409 22 AAI81346 Human polynucleoti
959 44 3.3 409 22 AAI85121 Human polynucleoti
960 44 3.3 409 22 AAI90784 Human polynucleoti
961 44 3.3 410 22 AAI83503 Human polynucleoti
962 44 3.3 410 22 AAI84857 Human polynucleoti
963 44 3.3 410 22 AAI90395 Human polynucleoti
964 44 3.3 410 22 AAI92307 Human polynucleoti
965 44 3.3 410 22 AAI81795 Human secreted pro
966 44 3.3 410 23 AAI54332 Human prostate exp
967 44 3.3 410 25 ABX74223 Aparagus cDNA enco
968 44 3.3 410 25 ABX39273 Bovine EST associa
969 44 3.3 411 22 AAI82241 Human polynucleoti
970 44 3.3 411 22 AAI84864 Human polynucleoti
971 44 3.3 411 22 AAI87361 Human polynucleoti
972 44 3.3 411 22 AAI87378 Human polynucleoti
973 44 3.3 411 22 AAI87998 Human polynucleoti
974 44 3.3 411 22 AAI91179 Human polynucleoti
975 44 3.3 412 22 AAI80754 Human polynucleoti
976 44 3.3 412 22 AAI84848 Human polynucleoti
977 44 3.3 412 22 AAI87374 Human polynucleoti
978 44 3.3 412 22 AAI87443 Human polynucleoti
979 44 3.3 412 22 AAI87923 Human polynucleoti
980 44 3.3 412 23 ABV48550 Human prostate exp
981 44 3.3 412 23 ABV54282 Human prostate exp
982 44 3.3 412 23 ABV56372 Human prostate exp
983 44 3.3 412 23 ABV56553 Human prostate exp
984 44 3.3 412 23 ABV57988 Human prostate exp
985 44 3.3 413 22 AAI82940 Human polynucleoti
986 44 3.3 413 22 AAI85119 Human polynucleoti
987 44 3.3 413 22 AAI85186 Human polynucleoti
988 44 3.3 413 22 AAI89034 Human polynucleoti
989 44 3.3 413 24 ABL49494 Sequence #96 used
990 44 3.3 413 24 ABL77265 Human ovarian canc
991 44 3.3 413 24 ABK30684 Plant dwarfing/stu
992 44 3.3 415 22 AAI92174 Human polynucleoti
993 44 3.3 416 22 AAI87993 Human polynucleoti
994 44 3.3 416 25 ABX36081 Bovine EST associa
995 44 3.3 416 25 ABX39419 Bovine EST associa
996 44 3.3 417 20 AAZ24888 Human secreted pro
997 44 3.3 417 23 ABV04722 Human prostate exp
998 44 3.3 417 25 ACC50754 Human secreted pro
999 44 3.3 417 25 ABZ71417 Secreted protein-e
1000 44 3.3 418 22 AAI88540 Human polynucleoti
```

ALIGNMENTS

```
RESULT 1
AAZ28358
ID AAZ28358 standard; DNA; 3375 BP.
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XX AC AAZ28358;
```

```
XX DT 18-JUN-1999 (first entry)
```

```
XX DE Human Stat6 coding sequence.
```

```
XX Stat6; Stat6b; human; signal transducers and activators of transcription;
KW isoform: myeloid cancer; asthma; sarcoma; scleroderma; fibrotic disease;
KW bone marrow fibrosis; AIDS; Stat6c; ss.
```

```
XX OS Homo sapiens.
```

```
XX PN WO9910493-A1.
```

```
XX PD 04-MAR-1999.
```

```
XX PF 27-AUG-1998; 98WO-US17821.
```

```
XX PR 05-JAN-1998; 98US-0070397.
```

```
XX PR 27-AUG-1997; 97US-0056075.
```

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XX
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```
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
```

```
XX Larochele WJ, Patel B, Pierce JH;
```

```
XX WPI; 1999-214517/18.
```

```
DR P-PSDB; AAY05223.
```

```
XX New isoforms of Stat6 - having differential effects on the
PT modulation of Stat6 activity in cells
```

```
XX Disclosure; Page 79-83; 88pp; English.
```

```
PS This sequence encodes human Stat6 (signal transducers and activators
XX of transcription). The invention relates to attenuated and dominant
CC negative isoforms of human Stat6. The detection and quantitation of DNA
CC or mRNA encoding Stat6 and/or Stat6b and/or Stat6c can be used to detect
CC differential expression of Stat6 isoforms in numerous diseases, including
CC myeloid cancer, asthma, sarcoma, scleroderma, bone marrow fibrosis,
CC fibrotic diseases and AIDS. The nucleic acids can be used to screen
CC genomic or cDNA libraries or to identify complementary sequences. The
CC identification of the genetic locus of the Stat6 gene can be used for
CC detection of chromosomal aberrations and translocations involving the
CC Stat6 gene. Antibodies against the isoforms can be used to detect the
CC presence of Stat6 and/or Stat6b and/or Stat6c in a sample. Because of the
CC variation of the roles of Stat6b and Stat6c in regulating gene
CC transcription the isolated and purified forms can be used to study gene
CC regulation and in screening assays for identifying drug candidates which
CC may be used as agonists or antagonists. The two polypeptides may also be
CC used in gene therapy protocols. In particular, Stat6b and/or Stat6c can
CC therapeutically modulate the development and differentiation of B and
CC T cells and can enhance IL-4 immunological function in immunocompromised
CC individuals. Stat6 activation correlates with functional responses
CC induced by interleukin-4 (IL-4), IL-13 and platelet-derived growth factor
CC (PDGF). Stat6b when compared Stat6 is an attenuated regulator of gene
CC transcription. Stat6c is a dominant negative regulator of gene
XX transcription.
```

```
XX SQ Sequence 3375 BP; 802 A; 967 C; 943 G; 663 T; 0 other;
```

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Query Match 3.8%; Score 50; DB 20; Length 3375;
```

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Best Local Similarity 100.0%; Pred. No. 2.3e-08;
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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1277 TTGCTGTAAAAA 1326
```

```
Db 3318 TTGCTGTAAAAA 3367
```

```
RESULT 2
```

```
AAZ01230
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```
ID AAZ01230 standard; cDNA; 1522 BP.
```

```
XX AC AAZ01230;
```

```
XX DT 04-OCT-2000 (first entry)
```

```
XX DE Maize Rad23 protein #1 encoding cDNA.
```

```
XX Rad23; maize; ATCC No: PTA-530; recombinant expression cassette; wheat;
KW transgenic plant; soybean; sunflower; sorghum; canola; modulator; ss.
```

```
XX Zea mays.
```

```
XX Key Location/Qualifiers
```

```
XX CDS 58..1275
```

```
XX FT /*tag= a
```

```
XX FT /product= "Maize Rad23 protein #1"
```

```
XX FT /note= "Contained in ATCC No: PTA-530"
```

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XX WO200031268-A1.
```

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XX PD 02-JUN-2000.
```

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XX
```

```
PF 12-OCT-1999; 99WO-US24129.
XX
PR 23-NOV-1998; 98US-0109728.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Mahajan PB, Tagliani L;
PI
XX WPI; 2000-400078/34.
XX
XX P-PSDB; AAY71458.
XX
XX Isolated nucleic acid encoding maize RAD23 protein is used to modulate
PT the levels of polypeptides in plant or in assays for identifying
PT compounds that bind to and/or increase/decrease enzymatic activity of
PT catalytically active polypeptides -
XX
XX Claim 1e; Page 73-75; 82pp; English.
XX
XX The present sequence is the cDNA encoding maize Rad23 protein #1. It is
CC isolated from V5 root tissue of a Zea mays cell line B73, infested with
CC corn root worm. This cDNA is deposited under the ATCC No: PTA-530. Maize
CC Rad23 DNA sequence operably linked to a promoter can be used to construct
CC a recombinant expression cassette. This expression cassette can be used
CC to generate a dicot or monocot transgenic plant e.g., maize, soybean,
CC sunflower, sorghum, canola, wheat, etc., It can also be used to modulate
CC the levels of Rad23 polypeptide expression in a plant or in assays to
CC identify compounds, that bind to and/or modulate the enzymatic activity
CC of catalytically active polypeptides.
XX
XX Sequence 1522 BP; 430 A; 375 C; 370 G; 347 T; 0 other;
SQ
Query Match 3.6%; Score 48; DB 21; Length 1522;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1279 CGTGTAAAAA 1326
DB 1455 CGTGTAAAAA 1502
RESULT 3
AAA26365
ID AAA26365 standard; cDNA; 2227 BP.
XX
XX AAA26365;
AC
XX
XX 29-JUN-2000 (first entry)
DT
DE Human secreted protein gene 20 SEQ ID NO:30.
XX
XX Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW antiHIV; antiinflammatory; neutropic; neuroprotective; antiallergic;
KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
KW immune disease; inflammation; blood disorder; tumour; chromosome 5; ss.
XX
XX Homo sapiens.
OS
XX WO200006698-A1.
XX
XX 10-FEB-2000.
XX
XX 29-JUL-1999; 99WO-US17130.
XX
XX 30-JUL-1998; 98US-0094657.
PR 05-AUG-1998; 98US-0095486.
PR 06-AUG-1998; 98US-0095454.
PR 06-AUG-1998; 98US-0095455.
PR 12-AUG-1998; 98US-0096319.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
PI
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PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX
XX WPI; 2000-195282/17.
XX
XX P-PSDB; AAY91470.
XX
XX New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders -
XX
XX Claim 1; Page 386; 634pp; English.
XX
XX The polynucleotide sequences given in AAA26346 to AAA26458 encode the
CC human secreted proteins given in AAY91451 to AAY91691. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic;
CC immunosuppressive; antiHIV; antiinflammatory; antibacterial; antidiabetic;
CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
CC corresponding secreted proteins are useful for preventing, treating or
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
CC pathological conditions can be diagnosed by determining the amount of the
CC proteins in a sample or by determining the presence of mutations in the
CC polynucleotides. Specific uses are described for each of the
CC polynucleotides, based on which tissues they are most highly expressed
CC in, and include developing products for the diagnosis or treatment of
CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
CC and fetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation,
CC allergies, Alzheimer's and behavioural disorders, schizophrenia,
CC osteoporosis, arthritis, infections, AIDS, spinal cord injuries,
CC transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,
CC cardiovascular disorders, reproductive disorders, gastrointestinal
CC disorders, respiratory disorders and metabolic disorders. The proteins
CC or polynucleotides can also be used as food additives or preservatives.
CC The proteins are also useful for identifying their binding partners.
CC AAA26337 to AAA26345 and AAY91450 are sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 2227 BP; 544 A; 539 C; 553 G; 570 T; 21 other;
SQ
Query Match 3.6%; Score 48; DB 21; Length 2227;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1279 CGTGTAAAAA 1326
DB 2179 CGTGTAAAAA 2226
RESULT 4
AAH34842
ID AAH34842 standard; cDNA; 2227 BP.
XX
XX AAH34842;
AC
XX
XX 03-SEP-2001 (first entry)
DT
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1924.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
XX Homo sapiens.
OS
XX WO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-US26524.
XX
XX 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
PR
```

(HUMA-) HUMAN GENOME SCI INC.
Ruben SM, Barash SC, Birse CE, Rosen CA;
WFI; 2001-235357/24.
P-PSDB; AAG75437.
Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
useful for preventing, diagnosing and/or treating colorectal cancers -
Claim 1; Page 3434-3435; 9803pp; English.
AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
cancer-associated nucleic acid molecules (N) and proteins (P), where
the proteins are collectively known as colon cancer antigens. The colon
cancer antigens have cytostatic activity and can be used in gene
therapy and vaccine production. N and P may be used in the prevention,
diagnosis and treatment of diseases associated with inappropriate P
expression. For example, N and P may be used to treat disorders
associated with decreased expression by rectifying mutations or deletions
in a patient's genome that affect the activity of P by expressing
inactive proteins or to supplement the patients own production of P.
Additionally, N may be used to produce the colon cancer-associated ps,
by inserting the nucleic acids into a host cell and culturing the cell
to express the proteins. N and P can be used in the prevention, diagnosis
and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
and AAB77789 represent sequences used in the exemplification of the
present invention.
N.B. Pages 666 to 682 and page 7053 of the sequence listing were
missing at time of publication, meaning no sequences are present for
SEQ ID NO:1027 to 1052, 7921 and 7922.
Sequence 2227 BP; 544 A; 539 C; 553 G; 570 T; 21 other;

Query Match 3.6%; Score 48; DB 22; Length 2227;
 Best Local Similarity 100.0%; Pred. No. 1.12e-07;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1279 CGTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326
 |||||
 DB 2179 CGTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2226

RESULT 5
 ACC50729
 ID ACC50729 standard; cDNA; 2227 BP.
 XX
 AC ACC50729;
 XX
 XX 12-JUN-2003 (first entry)
 XX
 XX Human secreted protein coding sequence, SEQ ID 396.
 DE
 XX
 XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
 KW
 KW vulnery; antiinflammatory; nootropic; neuroprotective;
 KW antiparkinsonian; gene therapy; human; cardiovascular disorder;
 KW gene; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200295010-A2.
 FN
 XX
 XX 28-NOV-2002.
 PD
 XX
 XX 19-MAR-2002; 2002WO-US09785.
 PF
 XX
 XX 21-MAR-2001; 2001US-277340P.
 PR
 XX 19-JUL-2001; 2001US-306171P.
 XX 13-NOV-2001; 2001US-331287P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX

Rosen CA, Ruben SM;
WPI; 2003-129429/12.

Novel human secreted proteins, useful for detecting, preventing,
diagnosing, prognosticating, treating and/or ameliorating
cardiovascular disorders such as arrhythmia -

Claim 21; SEQ ID 396; 1881pp; English.

The present invention relates to novel human secreted proteins
(ABR71633-ABR48145) and their coding sequences (ACC50344-ACC50856). The
proteins and their coding sequences are useful for the preparation of a
diagnostic or pharmaceutical composition for diagnosing or treating a
cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest,
coronary arteriosclerosis and myocardial ischemia), neural disorders,
immune system disorders, muscular disorders, reproductive disorders,
gastrointestinal disorders, pulmonary disorders, renal disorders,
proliferative disorders and/or cancerous diseases and conditions, for
wound healing and epithelial cell proliferation, to treat inflammation or
infection, for treating thrombosis and arteriosclerosis, for treating or
preventing neural damage which occurs in neuronal disorders or
neurodegenerative conditions such as Alzheimer's disease and Parkinson's
disease, to enhance bone and periodontal regeneration and aid in tissue
transplants or bone grafts, to prevent skin aging or hair loss, to
stimulate growth and differentiation of haematopoietic cells and bone
marrow cells when used in combination with other cytokines, to maintain
organs before transplantation or for supporting cell culture of primary
tissues, to increase or decrease differentiation or proliferation of
embryonic stem cells, or to modulate mammalian characteristics or
metabolism.
Note: The sequence data for this patent was published in electronic
format and is available from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

Sequence 2227 BP; 544 A; 539 C; 553 G; 570 T; 21 other;

Query Match 3.6%; Score 48; DB 25; Length 2227;
Best Local Similarity 100.0%; Pred.No. 1.2e-07;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1279 CGTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326
 |||.....
Db 2179 CGTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2226

RESULT 6

ID ABZ71405

XX ABZ71405 standard; cDNA; 2227 BP.

AC ABZ71405;

DT 04-APR-2003 (first entry)

DE Secreted protein-encoding gene 48 cDNA clone HPTDQ23, SEQ ID NO:226.

KW Human; secreted protein; digestive disorder; gastrointestinal disorder;
KW mouth; oesophagus; stomach; small intestine; large intestine; liver;
KW biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
KW immune disorder; inflammation; infection; wound healing; drug screening;
KW chromosome identification; chromosome mapping; cytostatic;
KW anti-inflammatory; immunosuppressive; vulnery; gene therapy; gene ss.

OS Homo sapiens.

XX WO200276488-A1.

PX 03-OCT-2002.

PP 19-MAR-2002; 2002WO-US08276.

PF 21-MAR-2001; 2001US-277340P.

PR 19-JUL-2001; 2001US-306171P.

PS Claim 1; SEQ ID NO 11201; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and

CC the encoded proteins (AAO0010-AAO3910) that exhibit activity relating to

CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and

CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and

CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 429 BP; 180 A; 63 C; 65 G; 121 T; 0 other;

Query Match 3.5%; Score 47; DB 22; Length 429;

Best Local Similarity 100.0%; Pred. NO. 3.8e-07;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTCTAAAAA 1326

DB 147 GTCTAAAAA 193

RESULT 11

ABV48477

ID ABV48477 standard; cDNA; 439 BP.

XX

AC ABV48477;

XX

DT 17-SEP-2002 (first entry)

XX

DE Human prostate expression marker cDNA 48469.

XX

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

XX

OS Homo sapiens.

XX

XX WO200160860-A2.

XX

XX 23-AUG-2001.

XX

XX 20-FEB-2001; 2001WO-US05171.

XX

PR 17-FEB-2000; 2000US-183319P.

PR 16-MAR-2000; 2000US-189862P.

PR 25-MAY-2000; 2000US-207454P.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX

XX Schlegel R, Endege WO, Monahan JE;

PI

XX WPI; 2001-662795/76.

DR

XX Novel isolated nucleic acid molecule associated with cancerous state of

FT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer -

XX

PS Claim 1; Page 9503; 11750pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX

SQ Sequence 439 BP; 204 A; 81 C; 72 G; 82 T; 0 other;

Query Match 3.5%; Score 47; DB 23; Length 439;

Best Local Similarity 100.0%; Pred. NO. 3.7e-07;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA 1326

DB 131 GTGTAAAAA 177

RESULT 12

AAD42244

ID AAD42244 standard; cDNA; 902 BP.

XX

AC AAD42244;

XX

XX 04-NOV-2002 (first entry)

DT

XX

DE Corn FT homologue cDNA from clone p0104.cabak14rb.

XX

XX Floral developmental protein; flowering locus T; APETALA3; transgenic;

KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;

KW sterility; plant growth; inflorescence architecture; plant morphology;

XX tissue culture; cell division; corn; gene; ss.

XX

OS Zea mays.

XX

XX Key Location/Qualifiers

FH 90..611

CDS /*tag= a

FT /product= "Corn FT homologue protein"

FT

XX

XX WO200244390-A2.

XX

XX 06-JUN-2002.

XX

XX 21-NOV-2001; 2001WO-US43750.

XX

XX 28-NOV-2000; 2000US-253415P.

XX

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX

XX Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;

XX

XX WPI; 2002-547703/59.

DR

XX P-PSDB; AAE25742.

XX

XX New floral developmental polypeptide having flowering locus T or Ap3

FT homolog activity, useful for immunological screening of cDNA expression

PT libraries -

XX

PS Claim 6; Page 61; 88pp; English.

XX

CC The present invention relates to novel floral developmental proteins,

CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue

CC proteins and polynucleotides encoding such proteins. Floral developmental

CC polynucleotides are useful for transforming cells or for producing plants

CC by transforming the plant cells with the polynucleotides and regenerating

CC the plants from the transformed plant cells. Sequences of the invention

CC are useful for immunological screening of cDNA expression libraries. They

CC are also useful for creating transgenic plants. Polynucleotides of the

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 17:03:05 ; Search time 94 Seconds

(without alignments)

6226.320 Million cell updates/sec

Title: US-10-024-806-1

Perfect score: 1326

Sequence: 1 gcgcggagcttccaaagcc.....aaaaaaaaaaaaaaaaaaaa 1326

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Issued Patents NA.*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	48	3.6	1522	3	US-09-413-574-1
3	48	3.6	2227	4	US-09-489-847-30
4	47	3.5	1201	4	US-09-461-325-36
5	47	3.5	2671	6	5168051-9
6	46	3.5	347	1	US-08-104-072B-2
7	46	3.5	530	4	US-09-461-325-28
8	46	3.5	593	3	US-09-385-982-262
9	46	3.5	1660	4	US-09-461-325-129
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11	46	3.5	2002	4	US-09-819-993-1
12	46	3.5	2136	4	US-09-996-243-302
13	46	3.5	2196	4	US-09-149-476-163
14	46	3.5	2235	4	US-09-569-804-20
15	46	3.5	2625	3	US-09-245-041-18
16	46	3.5	2837	2	US-08-993-228-11
17	46	3.5	2897	2	US-08-927-394-1
18	46	3.5	2897	4	US-09-016-434-1163
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21	45	3.4	740	2	US-08-975-316-8
22	45	3.4	740	3	US-09-211-710-8
23	45	3.4	740	4	US-09-615-192A-8
24	45	3.4	741	2	US-08-975-316-58
25	45	3.4	741	4	US-09-615-192A-58
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53	45	3.3	80	4	US-09-284-627-23	Sequence 23, Appl
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56	44	3.3	120	2	US-08-151-477A-28	Sequence 28, Appl
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136	44	3.3	1174	2	US-08-872-437-1	Sequence 1, Appli	209	44	3.3	1701	4	US-09-996-243-114	Sequence 114, App
137	44	3.3	1174	3	US-08-651-136C-11	Sequence 11, Appl	210	44	3.3	1736	3	US-09-182-816-22	Sequence 22, Appl
138	44	3.3	1174	4	US-09-229-911A-11	Sequence 11, Appl	c 211	44	3.3	1736	3	US-09-182-816-24	Sequence 24, Appl
139	44	3.3	1181	1	US-08-181-271A-27	Sequence 27, Appl	212	44	3.3	1736	3	US-09-471-528-22	Sequence 22, Appl
140	44	3.3	1181	1	US-08-449-315-27	Sequence 27, Appl	c 213	44	3.3	1736	3	US-09-471-528-24	Sequence 24, Appl
141	44	3.3	1181	1	US-08-444-803-27	Sequence 27, Appl	214	44	3.3	1736	3	US-09-634-530-22	Sequence 22, Appl
142	44	3.3	1181	1	US-08-443-043-27	Sequence 27, Appl	c 215	44	3.3	1736	3	US-09-634-530-24	Sequence 24, Appl
143	44	3.3	1181	1	US-08-456-285A-27	Sequence 27, Appl	216	44	3.3	1737	1	US-08-202-056-4	Sequence 4, Appli
144	44	3.3	1181	1	US-08-455-416-27	Sequence 27, Appl	217	44	3.3	1737	1	US-08-076-093A-3	Sequence 3, Appli
145	44	3.3	1181	1	US-08-455-244-27	Sequence 27, Appl	218	44	3.3	1737	1	US-08-701-265-3	Sequence 3, Appli
146	44	3.3	1181	2	US-08-454-876-27	Sequence 27, Appl	219	44	3.3	1737	2	US-08-284-586-3	Sequence 3, Appli
147	44	3.3	1181	2	US-08-457-364-27	Sequence 27, Appl	220	44	3.3	1737	2	US-08-805-478-3	Sequence 3, Appli
148	44	3.3	1181	2	US-08-456-262-27	Sequence 27, Appl	221	44	3.3	1737	2	US-08-802-637A-3	Sequence 3, Appli
149	44	3.3	1181	2	US-08-456-240-27	Sequence 27, Appl	222	44	3.3	1737	2	US-08-801-238-3	Sequence 3, Appli
150	44	3.3	1181	2	US-08-455-736-27	Sequence 27, Appl	223	44	3.3	1737	2	US-08-801-228-3	Sequence 3, Appli
151	44	3.3	1181	2	US-08-971-217-27	Sequence 27, Appl	224	44	3.3	1737	3	US-09-104-296-3	Sequence 3, Appli
152	44	3.3	1181	3	US-09-350-600-27	Sequence 27, Appl	225	44	3.3	1737	5	PCT-US94-06380-2	Sequence 2, Appli
153	44	3.3	1190	4	US-09-390-207-1	Sequence 1, Appli	226	44	3.3	1738	3	US-08-379-482A-2	Sequence 2, Appli
154	44	3.3	1198	3	US-09-248-335-27	Sequence 27, Appl	227	44	3.3	1753	4	US-09-149-476-56	Sequence 56, Appl
155	44	3.3	1223	3	US-09-154-874-4	Sequence 4, Appli	228	44	3.3	1781	4	US-09-499-302A-1	Sequence 1, Appli
156	44	3.3	1223	4	US-08-931-668-4	Sequence 4, Appli	229	44	3.3	1781	4	US-09-618-512-1	Sequence 1, Appli
157	44	3.3	1242	3	US-08-413-974-1	Sequence 1, Appli	230	44	3.3	1817	1	US-08-473-981A-5	Sequence 5, Appli
158	44	3.3	1242	3	US-08-434-418-1	Sequence 1, Appli	231	44	3.3	1817	2	US-08-474-087-5	Sequence 5, Appli
159	44	3.3	1242	3	US-08-433-218-1	Sequence 1, Appli	232	44	3.3	1837	2	US-08-750-134A-4	Sequence 4, Appli
160	44	3.3	1242	3	US-08-174-739A-1	Sequence 1, Appli	233	44	3.3	1837	3	US-09-363-745-4	Sequence 4, Appli
161	44	3.3	1242	4	US-08-434-256-1	Sequence 1, Appli	234	44	3.3	1842	4	US-09-482-273-90	Sequence 90, Appl
162	44	3.3	1249	4	US-09-461-325-128	Sequence 128, App	235	44	3.3	1858	2	US-08-909-965C-11	Sequence 11, Appl
163	44	3.3	1260	4	US-09-461-325-93	Sequence 93, Appl	236	44	3.3	1878	4	US-09-465-558-39	Sequence 39, Appl
164	44	3.3	1281	4	US-09-436-521A-5	Sequence 5, Appli	237	44	3.3	1886	4	US-09-594-506-31	Sequence 31, Appl
165	44	3.3	1361	4	US-09-489-847-64	Sequence 64, Appl	238	44	3.3	1910	2	US-09-009-438-1	Sequence 1, Appli
166	44	3.3	1364	1	US-08-265-087-3	Sequence 3, Appli	239	44	3.3	1910	3	US-09-207-493-1	Sequence 2, Appli
167	44	3.3	1364	1	US-08-621-493-3	Sequence 3, Appli	240	44	3.3	1931	3	US-09-019-942-2	Sequence 2, Appli
168	44	3.3	1364	2	US-08-965-688-3	Sequence 3, Appli	241	44	3.3	1931	4	US-09-099-041A-1	Sequence 1, Appli
169	44	3.3	1364	3	US-09-260-173-3	Sequence 3, Appli	242	44	3.3	1931	4	US-09-245-281-1	Sequence 1, Appli
170	44	3.3	1370	4	US-09-026-408-12	Sequence 12, Appl	243	44	3.3	1931	4	US-09-470-371-2	Sequence 2, Appli
171	44	3.3	1371	4	US-09-026-408-1	Sequence 1, Appli	244	44	3.3	1931	4	US-09-207-359B-1	Sequence 1, Appli
172	44	3.3	1375	4	US-09-489-847-120	Sequence 120, App	245	44	3.3	1931	4	US-09-340-620A-1	Sequence 1, Appli
173	44	3.3	1376	4	US-09-489-847-66	Sequence 66, Appl	246	44	3.3	1934	3	US-08-776-844-1	Sequence 1, Appli

247	44	3.3	1934	4	US-09-909-325-1	Sequence 1, Appl	320	44	3.3	3994	4	US-09-738-946-7	Sequence 7, Appl
248	44	3.3	1951	4	US-09-465-558-35	Sequence 35, Appl	321	44	3.3	4931	3	US-08-726-320-2	Sequence 2, Appl
249	44	3.3	1963	4	US-09-482-373-91	Sequence 91, Appl	322	44	3.3	4931	3	US-09-208-716-2	Sequence 2, Appl
250	44	3.3	1964	3	US-08-468-856B-7	Sequence 7, Appl	323	44	3.3	5173	3	US-08-242-677-1	Sequence 1, Appl
251	44	3.3	1964	3	US-08-468-859A-7	Sequence 7, Appl	324	44	3.3	5503	2	US-08-726-012B-1	Sequence 1, Appl
252	44	3.3	1965	4	US-09-482-373-27	Sequence 27, Appl	325	44	3.3	6200	4	US-09-439-923-1	Sequence 1, Appl
253	44	3.3	1976	4	US-09-920-759-10	Sequence 10, Appl	326	44	3.3	6200	4	US-09-711-202A-1	Sequence 1, Appl
254	44	3.3	1998	3	US-09-232-200-68	Sequence 68, Appl	327	44	3.3	6200	4	US-09-711-205A-1	Sequence 1, Appl
255	44	3.3	1998	4	US-09-232-197-68	Sequence 68, Appl	328	44	3.3	6409	4	US-09-967-908A-1	Sequence 1, Appl
256	44	3.3	1998	4	US-09-232-201-68	Sequence 68, Appl	329	44	3.3	6638	2	US-08-070-301-2	Sequence 2, Appl
257	44	3.3	2026	4	US-08-932-228-3	Sequence 3, Appl	330	44	3.3	7724	4	US-08-486-049-1	Sequence 1, Appl
258	44	3.3	2060	4	US-09-345-473E-5	Sequence 5, Appl	331	44	3.3	10136	1	US-08-353-700-2	Sequence 2, Appl
259	44	3.3	2065	3	US-09-370-473-5	Sequence 5, Appl	332	44	3.3	10136	5	PCT-US95-16216-2	Sequence 2, Appl
260	44	3.3	2087	3	US-09-232-191-6	Sequence 6, Appl	333	44	3.3	12482	4	US-09-512-563C-25	Sequence 25, Appl
261	44	3.3	2087	4	US-09-232-200-6	Sequence 6, Appl	334	44	3.3	15450	4	US-09-470-661A-1	Sequence 1, Appl
262	44	3.3	2087	4	US-09-232-197-6	Sequence 6, Appl	335	44	3.3	50	1	US-08-420-443-1	Sequence 1, Appl
263	44	3.3	2087	4	US-09-232-201-6	Sequence 6, Appl	336	44	3.3	60	4	US-09-457-959-8	Sequence 8, Appl
264	44	3.3	2103	4	US-09-489-847-40	Sequence 40, Appl	337	44	3.3	61	4	US-09-457-959-7	Sequence 7, Appl
265	44	3.3	2179	4	US-09-370-838-152	Sequence 152, App	338	44	3.3	69	1	US-08-702-344-7	Sequence 7, Appl
266	44	3.3	2187	4	US-09-137-219B-2	Sequence 2, Appl	339	44	3.3	69	1	US-08-702-344-22	Sequence 22, Appl
267	44	3.3	2202	4	US-09-388-743-1	Sequence 1, Appl	340	44	3.3	71	4	US-09-816-089A-5	Sequence 5, Appl
268	44	3.3	2203	4	US-09-801-861-1	Sequence 1, Appl	341	44	3.3	80	1	US-07-920-281C-25	Sequence 25, Appl
269	44	3.3	2218	4	US-09-205-258-103	Sequence 103, App	342	44	3.3	80	3	US-08-466-277-25	Sequence 25, Appl
270	44	3.3	2230	3	US-08-378-313-24	Sequence 24, Appl	343	44	3.3	84	1	US-08-664-596B-3	Sequence 3, Appl
271	44	3.3	2239	4	US-09-196-390-1	Sequence 1, Appl	344	44	3.3	84	1	US-08-738-367-3	Sequence 3, Appl
272	44	3.3	2271	4	US-09-205-258-243	Sequence 243, App	345	44	3.3	90	1	US-08-677-944-1	Sequence 1, Appl
273	44	3.3	2276	4	US-09-205-258-183	Sequence 183, App	346	44	3.3	90	1	US-08-677-944-2	Sequence 2, Appl
274	44	3.3	2281	4	US-09-996-243-368	Sequence 368, App	347	44	3.3	90	3	US-09-065-058-16	Sequence 16, Appl
275	44	3.3	2301	3	US-09-232-191-8	Sequence 8, Appl	348	44	3.3	90	3	US-09-254-048A-1	Sequence 1, Appl
276	44	3.3	2301	3	US-09-232-200-8	Sequence 8, Appl	349	44	3.3	90	4	US-09-921-203-1	Sequence 1, Appl
277	44	3.3	2301	4	US-09-232-197-8	Sequence 8, Appl	350	44	3.3	90	4	US-09-816-089A-2	Sequence 2, Appl
278	44	3.3	2301	4	US-09-232-201-8	Sequence 20, Appl	351	44	3.3	91	4	US-09-404-879A-201	Sequence 201, App
279	44	3.3	2378	4	US-08-802-805D-20	Sequence 20, Appl	352	44	3.3	91	4	US-09-338-933-291	Sequence 291, App
280	44	3.3	2378	4	US-08-860-370-1	Sequence 1, Appl	353	44	3.3	91	4	US-09-215-681-201	Sequence 201, App
281	44	3.3	2399	3	US-08-860-370-1	Sequence 1, Appl	354	44	3.3	93	4	US-09-816-089A-8	Sequence 8, Appl
282	44	3.3	2405	1	US-08-484-087-30	Sequence 30, Appl	355	44	3.3	94	4	US-09-404-879A-261	Sequence 261, App
283	44	3.3	2405	3	US-08-185-359-30	Sequence 30, Appl	356	44	3.3	94	4	US-09-338-933-261	Sequence 261, App
284	44	3.3	2409	3	US-09-293-322C-8	Sequence 8, Appl	357	44	3.3	94	4	US-09-215-681-261	Sequence 261, App
285	44	3.3	2409	3	US-09-839-497A-8	Sequence 8, Appl	358	44	3.3	98	1	US-08-088-658-42	Sequence 42, Appl
286	44	3.3	2434	4	US-09-489-847-67	Sequence 67, Appl	359	44	3.3	98	2	US-08-471-907A-42	Sequence 42, Appl
287	44	3.3	2483	4	US-09-205-258-68	Sequence 68, Appl	360	44	3.3	100	3	US-08-991-789A-30	Sequence 30, Appl
288	44	3.3	2497	4	US-09-396-149-1	Sequence 1, Appl	361	44	3.3	100	4	US-09-062-451-30	Sequence 30, Appl
289	44	3.3	2550	6	5258287-23	Patent No. 5258287	362	44	3.3	100	4	US-09-598-326-30	Sequence 30, Appl
290	44	3.3	2589	3	US-08-569-749-1	Sequence 1, Appl	363	44	3.3	100	4	US-09-289-198-30	Sequence 30, Appl
291	44	3.3	2589	5	PCT-US96-12860-1	Sequence 1, Appl	364	44	3.3	101	4	US-09-404-879A-293	Sequence 293, App
292	44	3.3	2710	3	US-09-232-200-44	Sequence 44, Appl	365	44	3.3	101	4	US-09-338-933-293	Sequence 293, App
293	44	3.3	2710	3	US-09-232-200-70	Sequence 70, Appl	366	44	3.3	101	4	US-09-215-681-293	Sequence 293, App
294	44	3.3	2710	4	US-09-232-197-44	Sequence 44, Appl	367	44	3.3	105	2	US-08-735-381-2	Sequence 2, Appl
295	44	3.3	2710	4	US-09-232-197-70	Sequence 70, Appl	368	44	3.3	105	3	US-09-183-619-1	Sequence 1, Appl
296	44	3.3	2710	4	US-09-232-201-44	Sequence 44, Appl	369	44	3.3	105	3	US-09-201-674-2	Sequence 2, Appl
297	44	3.3	2710	4	US-09-232-201-70	Sequence 70, Appl	370	44	3.3	111	3	US-09-297-535-23	Sequence 23, Appl
298	44	3.3	2719	3	US-08-706-216-1	Sequence 1, Appl	371	44	3.3	117	1	US-08-702-344-3	Sequence 3, Appl
299	44	3.3	2760	1	US-08-101-593-1	Sequence 1, Appl	372	44	3.3	121	3	US-09-297-535-20	Sequence 20, Appl
300	44	3.3	2760	1	US-08-101-593-3	Sequence 3, Appl	373	44	3.3	121	3	US-08-330-108-16	Sequence 16, Appl
301	44	3.3	2773	4	US-09-996-243-178	Sequence 178, App	374	44	3.3	198	5	PCT-US92-10087-16	Sequence 16, Appl
302	44	3.3	2790	3	US-08-800-291B-1	Sequence 1, Appl	375	44	3.3	199	4	US-09-702-705-102	Sequence 102, App
303	44	3.3	2821	4	US-09-702-705-1669	Sequence 1669, Ap	376	44	3.3	199	4	US-09-736-457-102	Sequence 37, Appl
304	44	3.3	2821	4	US-09-736-457-1669	Sequence 1669, Ap	377	44	3.3	208	1	US-08-686-878A-37	Sequence 37, Appl
305	44	3.3	2908	4	US-09-930-181-1	Sequence 1, Appl	378	44	3.3	208	4	US-09-175-928-37	Sequence 37, Appl
306	44	3.3	3001	4	US-09-539-333D-153	Sequence 153, App	379	44	3.3	227	2	US-08-520-678A-28	Sequence 28, Appl
307	44	3.3	3214	1	US-08-484-105-17	Sequence 17, Appl	380	44	3.3	227	2	US-08-897-126-28	Sequence 28, Appl
308	44	3.3	3214	1	US-08-484-106-17	Sequence 17, Appl	381	44	3.3	227	3	US-09-191-136-29	Sequence 29, Appl
309	44	3.3	3410	3	US-09-020-956-110	Sequence 110, App	382	44	3.3	237	3	US-08-520-678A-25	Sequence 25, Appl
310	44	3.3	3410	3	US-09-030-607-110	Sequence 110, App	383	44	3.3	253	2	US-08-897-126-25	Sequence 25, Appl
311	44	3.3	3410	4	US-09-439-313-110	Sequence 110, App	384	44	3.3	257	2	US-08-520-678A-24	Sequence 24, Appl
312	44	3.3	3410	4	US-09-353-616A-110	Sequence 110, App	385	44	3.3	257	3	US-08-897-126-24	Sequence 24, Appl
313	44	3.3	3410	4	US-09-602-877A-100	Sequence 100, App	386	44	3.3	260	2	US-08-520-678A-29	Sequence 29, Appl
314	44	3.3	3410	4	US-09-232-149A-110	Sequence 110, App	387	44	3.3	260	3	US-08-897-126-29	Sequence 29, Appl
315	44	3.3	3437	3	US-08-860-339-17	Sequence 17, Appl	388	44	3.3	263	4	US-09-091-097-26	Sequence 26, Appl
316	44	3.3	3527	2	US-08-909-985C-7	Sequence 7, Appl	389	44	3.3	270	2	US-08-520-678A-30	Sequence 30, Appl
317	44	3.3	3581	2	US-08-738-349-1	Sequence 1, Appl	390	44	3.3	270	3	US-08-897-126-30	Sequence 30, Appl
318	44	3.3	3602	4	US-09-403-929-1	Sequence 1, Appl	391	44	3.3	271	2	US-08-731-272A-29	Sequence 29, Appl
319	44	3.3	3772	4	US-09-996-243-61	Sequence 61, Appl	392	44	3.3	337	2	US-09-032-684-11	Sequence 11, Appl

C 393	43	3.2	350	1	US-08-171-385-14	Sequence 14, Appl	466	43	3.2	879	1	US-08-158-682A-1	Sequence 1, Appl
C 394	43	3.2	350	2	US-08-361-441B-14	Sequence 14, Appl	467	43	3.2	879	1	US-08-015-203-1	Sequence 1, Appl
C 395	43	3.2	356	2	US-08-520-678A-22	Sequence 22, Appl	468	43	3.2	882	2	US-08-909-965C-9	Sequence 9, Appl
C 396	43	3.2	356	3	US-08-897-126-22	Sequence 22, Appl	469	43	3.2	888	3	US-09-188-910-13	Sequence 13, Appl
C 397	43	3.2	427	4	US-09-461-325-107	Sequence 107, App	470	43	3.2	888	4	US-09-312-283C-13	Sequence 13, Appl
C 398	43	3.2	441	4	US-09-601-537-10	Sequence 10, Appl	471	43	3.2	898	4	US-09-857-556A-29	Sequence 29, Appl
C 399	43	3.2	467	2	US-08-841-349-18	Sequence 18, Appl	472	43	3.2	917	4	US-09-227-357-43	Sequence 43, Appl
C 400	43	3.2	470	3	US-09-020-956-102	Sequence 102, App	473	43	3.2	921	4	US-09-227-357-30	Sequence 30, Appl
C 401	43	3.2	470	3	US-09-030-607-102	Sequence 102, App	474	43	3.2	931	4	US-09-482-273-31	Sequence 31, Appl
C 402	43	3.2	470	4	US-09-439-313-102	Sequence 102, App	475	43	3.2	940	2	US-08-471-717-1	Sequence 1, Appl
C 403	43	3.2	470	4	US-09-352-616A-102	Sequence 102, App	476	43	3.2	941	4	US-09-205-258-186	Sequence 186, App
C 404	43	3.2	470	4	US-09-232-149A-102	Sequence 102, App	477	43	3.2	949	4	US-09-489-847-35	Sequence 35, Appl
C 405	43	3.2	472	4	US-09-205-258-130	Sequence 130, App	478	43	3.2	953	1	US-08-197-793-1	Sequence 1, Appl
C 406	43	3.2	474	3	US-08-516-859A-97	Sequence 97, Appl	479	43	3.2	953	1	US-08-636-176-1	Sequence 1, Appl
C 407	43	3.2	474	4	US-09-586-472-97	Sequence 97, Appl	480	43	3.2	953	5	PCT-US95-01618-1	Sequence 1, Appl
C 408	43	3.2	474	4	US-09-528-706-97	Sequence 97, Appl	481	43	3.2	960	3	US-09-248-335-57	Sequence 57, Appl
C 409	43	3.2	485	4	US-09-996-243-245	Sequence 245, App	482	43	3.2	967	3	US-09-248-335-51	Sequence 51, Appl
C 410	43	3.2	495	4	US-09-220-132-186	Sequence 186, App	483	43	3.2	972	1	US-07-915-934-1	Sequence 1, Appl
C 411	43	3.2	509	3	US-09-030-607-202	Sequence 202, App	484	43	3.2	972	1	US-08-325-743-1	Sequence 1, Appl
C 412	43	3.2	509	4	US-09-439-313-202	Sequence 202, App	485	43	3.2	972	4	US-09-549-831-5	Sequence 5, Appl
C 413	43	3.2	509	4	US-09-352-616A-202	Sequence 202, App	486	43	3.2	972	4	US-09-996-243-358	Sequence 358, App
C 414	43	3.2	509	4	US-09-232-149A-202	Sequence 202, App	487	43	3.2	974	2	US-08-504-459-13	Sequence 13, Appl
C 415	43	3.2	536	1	US-08-341-568-1	Sequence 1, Appl	488	43	3.2	974	2	US-09-381-488-6	Sequence 6, Appl
C 416	43	3.2	536	2	US-08-911-020-1	Sequence 1, Appl	489	43	3.2	985	4	US-09-322-409-25	Sequence 25, Appl
C 417	43	3.2	537	4	US-09-720-201A-4	Sequence 4, Appl	490	43	3.2	985	4	US-09-322-409-27	Sequence 27, Appl
C 418	43	3.2	551	4	US-09-996-243-166	Sequence 166, App	491	43	3.2	985	4	US-09-451-527-25	Sequence 25, Appl
C 419	43	3.2	552	4	US-09-461-325-111	Sequence 111, App	492	43	3.2	985	4	US-09-451-527-27	Sequence 27, Appl
C 420	43	3.2	569	4	US-09-461-325-44	Sequence 44, Appl	493	43	3.2	1001	1	US-08-728-259A-10	Sequence 10, Appl
C 421	43	3.2	570	4	US-09-996-243-407	Sequence 407, App	494	43	3.2	1001	2	US-08-473-486-10	Sequence 10, Appl
C 422	43	3.2	572	4	US-09-342-653-5	Sequence 5, Appl	495	43	3.2	1013	1	US-07-920-619-30	Sequence 30, Appl
C 423	43	3.2	577	3	US-09-385-982-203	Sequence 203, App	496	43	3.2	1013	1	US-08-086-410-23	Sequence 23, Appl
C 424	43	3.2	578	4	US-09-602-877A-95	Sequence 95, Appl	497	43	3.2	1013	1	US-08-314-586-30	Sequence 30, Appl
C 425	43	3.2	588	4	US-09-205-258-64	Sequence 64, Appl	498	43	3.2	1013	4	US-09-322-409-6	Sequence 6, Appl
C 426	43	3.2	593	4	US-09-904-615-59	Sequence 59, Appl	499	43	3.2	1013	4	US-09-322-409-8	Sequence 8, Appl
C 427	43	3.2	615	4	US-09-105-542A-2	Sequence 2, Appl	500	43	3.2	1013	4	US-09-451-527-6	Sequence 6, Appl
C 428	43	3.2	619	4	US-09-489-847-58	Sequence 58, Appl	501	43	3.2	1013	4	US-09-451-527-8	Sequence 8, Appl
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C 430	43	3.2	635	1	US-08-455-633A-35	Sequence 35, Appl	503	43	3.2	1023	1	US-08-252-966B-16	Sequence 16, Appl
C 431	43	3.2	635	1	US-08-416-336-5	Sequence 5, Appl	504	43	3.2	1023	4	US-09-229-947-38	Sequence 38, Appl
C 432	43	3.2	635	2	US-08-456-460C-35	Sequence 35, Appl	505	43	3.2	1029	4	US-09-216-393B-11	Sequence 11, Appl
C 433	43	3.2	635	5	PCT-US94-05354-35	Sequence 35, Appl	506	43	3.2	1032	4	US-09-257-179-21	Sequence 21, Appl
C 434	43	3.2	636	4	US-09-594-508-27	Sequence 27, Appl	507	43	3.2	1036	4	US-09-205-258-86	Sequence 86, Appl
C 435	43	3.2	639	4	US-09-482-273-49	Sequence 49, Appl	508	43	3.2	1037	4	US-09-489-847-112	Sequence 112, App
C 436	43	3.2	644	4	US-09-996-243-282	Sequence 282, App	509	43	3.2	1039	4	US-09-464-535-23	Sequence 23, Appl
C 437	43	3.2	644	4	US-09-720-201A-6	Sequence 6, Appl	510	43	3.2	1046	1	US-08-361-467B-4	Sequence 4, Appl
C 438	43	3.2	664	4	US-09-904-615-66	Sequence 66, Appl	511	43	3.2	1046	1	US-08-489-847-38	Sequence 38, Appl
C 439	43	3.2	674	4	US-09-620-405B-465	Sequence 465, App	512	43	3.2	1048	4	US-09-489-847-38	Sequence 38, Appl
C 440	43	3.2	674	4	US-09-433-828B-465	Sequence 465, App	513	43	3.2	1050	4	US-09-482-273-58	Sequence 58, Appl
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C 461	43	3.2	857	1	US-08-730-163-1	Sequence 1, Appl	534	43	3.2	1212	4	US-09-149-476-186	Sequence 186, App
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794 43 3.2 2606 4 US-09-234-827B-3 Sequence 3, Appl
795 43 3.2 2608 4 US-09-904-615-16 Sequence 16, Appl
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806 43 3.2 2665 4 US-08-971-089-5 Sequence 5, Appl
807 43 3.2 2668 4 US-09-370-838-156 Sequence 156, App
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815 43 3.2 2797 4 US-09-482-273-74 Sequence 74, Appl
816 43 3.2 2806 4 US-09-653-839-9 Sequence 9, Appl
817 43 3.2 2845 4 US-09-996-243-230 Sequence 230, App
818 43 3.2 2851 4 US-09-535-521-1 Sequence 1, Appl
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822 43 3.2 2877 4 US-09-235-103-1 Sequence 1, Appl
823 43 3.2 2880 3 US-09-115-954-3 Sequence 3, Appl
824 43 3.2 2908 4 US-09-904-615-35 Sequence 35, Appl
825 43 3.2 2943 4 US-09-404-879A-38 Sequence 38, App
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830 43 3.2 3040 1 US-08-446-794A-1 Sequence 1, Appl

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979	42	3.2	1868	4	US-09-676-6108-26	Sequence 26, Appl
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991	42	3.2	3134	4	US-09-022-765-1	Sequence 1, Appli
992	42	3.2	3134	4	US-09-551-974A-1	Sequence 1, Appli
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996	42	3.2	3637	3	US-08-445-461-3	Sequence 3, Appli
997	42	3.2	4235	4	US-09-702-705-317	Sequence 317, App
998	42	3.2	4235	4	US-09-736-457-317	Sequence 317, App
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RESULT 4

US-09-461-325-36
; Sequence 36, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029FI
; CURRENT APPLICATION NUMBER: US/09/461,325A
; EARLIER FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: SITE
; LOCATION: (29)
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; OTHER INFORMATION: n equals a.t.g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (63)
; OTHER INFORMATION: n equals a.t.g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1201)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-461-325-36

Query Match 3.5%; Score 47; DB 4; Length 1201;
Best Local Similarity 100.0%; Pred. No. 5.1e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1131 GTGTAAGAAAAA 1177

RESULT 5

5168051-9
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO: 9
; LENGTH: 2671

Query Match 3.5%; Score 47; DB 6; Length 2671;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2577 GTGTAAGAAAAA 2623

RESULT 6

US-08-104-072B-2
; Sequence 2, Application US/08104072B
; Patent No. 5639948
; GENERAL INFORMATION:
; APPLICANT: Michiels, Frank
; APPLICANT: Morioka, Sinji
; APPLICANT: Scheirlinck, Trees
; APPLICANT: Komari, Toshihiko
; TITLE OF INVENTION: Stamen-specific Promoters from Rice
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5639948west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,072B
; FILING DATE: 05-AUG-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 9200272
; FILING DATE: 06-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91403352.7
; FILING DATE: 10-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91402590.3
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91400318.1
; FILING DATE: 08-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 8076.93USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: rice
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; OTHER INFORMATION: /product= "cDNA T23"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 333..347
; OTHER INFORMATION: /product= "cloning adaptor
; OTHER INFORMATION: sequence"
US-08-104-072B-2

Query Match 3.5%; Score 46; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
Db 284 TGTAAAAA 329

RESULT 7

US-09-461-325-28
; Sequence 28, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-325-28

Query Match 3.5%; Score 46; DB 4; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
Db 470 TGTAAAAA 515

RESULT 8

US-09-385-982-262/c
; Sequence 262, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGS, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 262
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(593)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-262

Query Match 3.5%; Score 46; DB 3; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
Db 75 TGTAAAAA 30

RESULT 9

US-09-461-325-129
; Sequence 129, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 129
; LENGTH: 1660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-325-129

Query Match 3.5%; Score 46; DB 4; Length 1660;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
Db 1615 TGTAAAAA 1660

RESULT 10

US-09-801-052-1
; Sequence 1, Application US/09801052
; Patent No. 6368642
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; FILE REFERENCE: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001045
; CURRENT APPLICATION NUMBER: US/09/801,052
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1872
; TYPE: DNA

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; ORGANISM: Human
US-09-801-052-1

Query Match      3.5%; Score 46; DB 4; Length 1872;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
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Db 1765 TGTAAAAA 1810

RESULT 11
US-09-819-993-1
; Sequence 1, Application US/09819993
; Patent No. 6436692
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; FILE REFERENCE: CLO01195
; CURRENT APPLICATION NUMBER: US/09/819,993
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2002
; TYPE: DNA
; ORGANISM: Human
US-09-819-993-1

Query Match      3.5%; Score 46; DB 4; Length 2002;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1281 TGTAAAAA 1326
    |||||
Db 1956 TGTAAAAA 2001

RESULT 12
US-09-996-243-302
; Sequence 302, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C13
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
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; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
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; PRIOR APPLICATION NUMBER: 60/090445
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
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; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 3.5%; Score 46; DB 4; Length 2136;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1281 TGTAAA 1326
Db 2061 TGTAAA 2106

RESULT 13

US-09-149-476-163
; Sequence 163, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002PI
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617

7	EARLIER APPLICATION NUMBER: 60/056,882
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,637
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,903
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,888
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,879
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,880
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,894
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,911
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,636
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,874
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,910
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,864
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,892
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/057,761
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/047,595
7	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/047,599
7	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/047,588
7	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/047,585
7	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/047,586
7	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/047,590
7	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/047,594
7	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/047,589
7	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/043,578
7	EARLIER FILING DATE: 1997-04-11
7	EARLIER APPLICATION NUMBER: 60/043,576
7	EARLIER FILING DATE: 1997-04-11
7	EARLIER APPLICATION NUMBER: 60/047,501
7	EARLIER FILING DATE: 1997-05-23
7	EARLIER APPLICATION NUMBER: 60/043,670
7	EARLIER FILING DATE: 1997-04-11
7	EARLIER APPLICATION NUMBER: 60/056,632
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,881
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,864
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,876
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,909
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,875
7	EARLIER FILING DATE: 1997-08-22
7	EARLIER APPLICATION NUMBER: 60/056,862
7	EARLIER FILING DATE: 1997-08-22

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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          3.5%; Score 46; DB 4; Length 2196;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1281 TGTAAAAA 1326
Db 2144 TGTAAAAA 2189
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RESULT 14

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US-09-569-804-20
; Sequence 20, Application US/09569804
; Patent No. 6506962
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; GENERAL INFORMATION:

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; APPLICANT: Bougri, Oleg
; APPLICANT: Rommens, Caius
; APPLICANT: Srivastava, Neelam
; APPLICANT: Swords, Kathleen M
; TITLE OF INVENTION: Acquired Resistance Genes in Plants
; FILE REFERENCE: 38-21(15415)
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; CURRENT APPLICATION NUMBER: US/09/569,804
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; CURRENT FILING DATE: 2000-05-12
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; PRIOR APPLICATION NUMBER: 60/133,965
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; PRIOR FILING DATE: 1999-05-13
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; NUMBER OF SEQ ID NOS: 36
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; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 20
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; LENGTH: 2235
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; TYPE: DNA
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; ORGANISM: Zea mays
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US-09-569-804-20
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Query Match          3.5%; Score 46; DB 4; Length 2235;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1281 TGTAAAAA 1326
Db 2176 TGTAAAAA 2221
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RESULT 15

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US-09-245-041-18
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; Sequence 18, Application US/09245041
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; Patent No. 6274339
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```
; GENERAL INFORMATION:
```

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; APPLICANT: Moore, K.
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; APPLICANT: Nagle, D.
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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS INCLUDING OBESITY
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; FILE REFERENCE: 7853-136
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; CURRENT APPLICATION NUMBER: US/09/245,041
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; CURRENT FILING DATE: 1999-02-05
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; EARLIER APPLICATION NUMBER: 60/093,630
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; EARLIER FILING DATE: 1998-07-21
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; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 18
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; LENGTH: 2625
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; TYPE: DNA
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; ORGANISM: Homo sapiens
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US-09-245-041-18
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Query Match          3.5%; Score 46; DB 3; Length 2625;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1281 TGTAAAAA 1326
Db 2574 TGTAAAAA 2619
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Search completed: November 7, 2003, 19:34:08
Job time : 108 secs
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46	3.5	2136	11	US-09-993-748-302	Sequence 302, App	164	46	3.5	2136	14	US-10-176-757-327	Sequence 227, App
46	3.5	2136	11	US-09-990-439-302	Sequence 302, App	165	46	3.5	2136	14	US-10-176-913-327	Sequence 227, App
46	3.5	2136	11	US-09-990-427-302	Sequence 302, App	166	46	3.5	2136	14	US-10-180-552-327	Sequence 227, App
46	3.5	2136	11	US-09-983-328-302	Sequence 302, App	167	46	3.5	2136	14	US-10-180-557-327	Sequence 227, App
46	3.5	2136	11	US-09-941-583-302	Sequence 302, App	168	46	3.5	2136	14	US-10-173-700-327	Sequence 227, App
46	3.5	2136	11	US-09-941-992-302	Sequence 302, App	169	46	3.5	2136	14	US-10-174-572-327	Sequence 227, App
46	3.5	2136	11	US-09-997-521-302	Sequence 302, App	170	46	3.5	2136	14	US-10-174-579-327	Sequence 227, App
46	3.5	2136	11	US-09-997-333-302	Sequence 302, App	171	46	3.5	2136	14	US-10-174-582-327	Sequence 227, App
46	3.5	2136	11	US-09-997-384-302	Sequence 302, App	172	46	3.5	2136	14	US-10-174-588-327	Sequence 227, App
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46	3.5	2136	11	US-09-997-614-302	Sequence 302, App	175	46	3.5	2136	14	US-10-175-743-327	Sequence 227, App
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46	3.5	2136	12	US-09-997-523-302	Sequence 227, App	178	46	3.5	2136	14	US-10-176-747-327	Sequence 227, App
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46	3.5	2136	12	US-10-194-457-227	Sequence 227, App	181	46	3.5	2136	14	US-10-176-987-327	Sequence 227, App
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5	46	3.5	2136	14	US-10-196-743-227	Sequence 227, App	348	46	3.5	2136	14	US-10-198-317-227	Sequence 227, App
6	46	3.5	2136	14	US-10-196-760-227	Sequence 227, App	349	46	3.5	2136	14	US-10-198-665-227	Sequence 227, App
7	46	3.5	2136	14	US-10-196-762-227	Sequence 227, App	350	46	3.5	2136	14	US-10-198-669-227	Sequence 227, App
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8	46	3.5	2136	14	US-10-176-753-227	Sequence 227, App	381	46	3.5	2136	14	US-10-197-707-227	Sequence 227, App
9	46	3.5	2136	14	US-10-176-917-227	Sequence 227, App	382	46	3.5	2136	14	US-10-197-707-227	Sequence 227, App

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529	46	3.5	2136	14	US-10-183-003-227	Sequence 227, App	C 602	45	3.4	308	10	US-09-954-531-263	Sequence 263, App
530	46	3.5	2136	14	US-10-183-016-227	Sequence 227, App	C 603	45	3.4	308	12	US-09-954-531-407	Sequence 407, App
531	46	3.5	2136	14	US-10-173-696-227	Sequence 227, App	C 604	45	3.4	365	10	US-09-960-352-5456	Sequence 5456, App
532	46	3.5	2136	14	US-10-125-9238-227	Sequence 227, App	C 605	45	3.4	444	10	US-09-960-352-1281	Sequence 1281, App
533	46	3.5	2136	14	US-10-176-491-227	Sequence 227, App	C 606	45	3.4	447	9	US-09-770-444-759	Sequence 759, App
534	46	3.5	2136	14	US-10-176-979-227	Sequence 227, App	C 607	45	3.4	450	11	US-09-918-995-12969	Sequence 12969, App
535	46	3.5	2136	14	US-10-187-592-227	Sequence 227, App	C 608	45	3.4	452	14	US-10-060-036-839	Sequence 839, App
536	46	3.5	2136	14	US-10-197-691-227	Sequence 227, App	C 609	45	3.4	456	10	US-09-960-352-5459	Sequence 5459, App
537	46	3.5	2136	14	US-10-198-771-227	Sequence 227, App	C 610	45	3.4	460	11	US-09-918-995-9458	Sequence 9458, App
538	46	3.5	2136	14	US-10-174-575A-227	Sequence 227, App	C 611	45	3.4	487	11	US-09-918-995-5922	Sequence 5922, App
539	46	3.5	2136	14	US-10-179-520-227	Sequence 227, App	C 612	45	3.4	524	9	US-09-797-207-5	Sequence 5, Appl
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541	46	3.5	2136	14	US-10-202-941-227	Sequence 227, App	C 614	45	3.4	550	12	US-09-814-353-11390	Sequence 11390, App
542	46	3.5	2136	14	US-10-205-910-227	Sequence 227, App	C 615	45	3.4	595	10	US-09-967-552A-31	Sequence 31, Appl
543	46	3.5	2136	14	US-10-179-526-227	Sequence 227, App	C 616	45	3.4	640	14	US-10-078-090-108	Sequence 108, App
544	46	3.5	2136	14	US-10-173-701-227	Sequence 227, App	C 617	45	3.4	690	14	US-10-106-698-943	Sequence 943, App
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547	46	3.5	2136	14	US-10-183-018-227	Sequence 227, App	C 620	45	3.4	741	15	US-10-174-693-8	Sequence 8, Appl
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549	46	3.5	2136	14	US-10-184-637-227	Sequence 227, App	C 622	45	3.4	756	10	US-09-950-9338-20	Sequence 20, Appl
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551	46	3.5	2136	14	US-10-197-706-227	Sequence 227, App	C 624	45	3.4	775	11	US-09-948-820-28	Sequence 28, Appl
552	46	3.5	2136	14	US-10-201-857-227	Sequence 227, App	C 625	45	3.4	780	14	US-10-102-806-150	Sequence 150, App
553	46	3.5	2136	14	US-10-202-413-227	Sequence 227, App	C 626	45	3.4	788	15	US-10-174-693-96	Sequence 96, Appl
554	46	3.5	2136	14	US-10-202-938-227	Sequence 227, App	C 627	45	3.4	907	9	US-09-873-585-3	Sequence 3, Appl
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557	46	3.5	2136	14	US-10-205-905-227	Sequence 227, App	C 630	45	3.4	958	9	US-09-925-301-412	Sequence 412, App
558	46	3.5	2136	14	US-10-206-918-227	Sequence 227, App	C 631	45	3.4	958	9	US-09-746-485A-5	Sequence 5, Appl
559	46	3.5	2136	14	US-10-208-025-227	Sequence 227, App	C 632	45	3.4	958	11	US-09-808-898-5	Sequence 5, Appl
560	46	3.5	2136	14	US-10-198-760-227	Sequence 227, App	C 633	45	3.4	958	14	US-10-126-139-5	Sequence 5, Appl
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562	46	3.5	2136	14	US-10-184-611-227	Sequence 227, App	C 635	45	3.4	958	14	US-10-126-777-5	Sequence 5, Appl
563	46	3.5	2136	14	US-10-187-739-227	Sequence 227, App	C 636	45	3.4	1018	13	US-10-078-929-151	Sequence 151, App
564	46	3.5	2136	14	US-10-206-907-227	Sequence 227, App	C 637	45	3.4	1041	10	US-09-945-300-440	Sequence 440, App
565	46	3.5	2136	14	US-10-183-009-227	Sequence 227, App	C 638	45	3.4	1054	14	US-10-180-375-109	Sequence 109, App
566	46	3.5	2136	14	US-10-187-755-227	Sequence 227, App	C 639	45	3.4	1077	10	US-09-764-868-497	Sequence 497, App
567	46	3.5	2136	14	US-09-809-391-163	Sequence 163, App	C 640	45	3.4	1093	9	US-09-925-301-219	Sequence 219, App
568	46	3.5	2136	14	US-09-882-171-163	Sequence 163, App	C 641	45	3.4	1119	11	US-09-786-753-133	Sequence 133, App
569	46	3.5	2235	14	US-10-318-780-20	Sequence 20, Appl	C 642	45	3.4	1143	11	US-09-809-391-119	Sequence 119, App
570	46	3.5	2479	12	US-10-321-802-17	Sequence 17, Appl	C 643	45	3.4	1143	12	US-09-882-171-119	Sequence 4, Appl
571	46	3.5	2527	9	US-09-925-302-253	Sequence 253, App	C 644	45	3.4	1178	9	US-09-952-689-4	Sequence 229, App
572	46	3.5	2611	14	US-10-097-340-108	Sequence 108, App	C 645	45	3.4	1186	11	US-09-822-846-229	Sequence 229, App
573	46	3.5	2625	10	US-09-893-238-18	Sequence 18, Appl	C 646	45	3.4	1212	14	US-10-112-267-34	Sequence 34, Appl
574	46	3.5	2892	14	US-09-960-706-980	Sequence 980, App	C 647	45	3.4	1212	14	US-10-112-267-35	Sequence 35, Appl
575	46	3.5	2924	14	US-10-163-198-26	Sequence 26, Appl	C 648	45	3.4	1233	14	US-10-102-806-256	Sequence 256, App
576	46	3.5	3005	10	US-09-962-678-1	Sequence 1, Appl	C 649	45	3.4	1257	9	US-09-925-301-188	Sequence 188, App
577	46	3.5	3376	10	US-09-834-975-775	Sequence 775, App	C 650	45	3.4	1300	9	US-09-822-849A-3	Sequence 3, Appl
578	46	3.5	3436	9	US-09-789-561-12	Sequence 12, Appl	C 651	45	3.4	1303	10	US-09-764-846-125	Sequence 125, App
579	46	3.5	3436	10	US-09-790-622-3	Sequence 3, Appl	C 652	45	3.4	1303	14	US-10-091-483-125	Sequence 125, App
580	46	3.5	3436	14	US-10-141-953-3	Sequence 3, Appl	C 653	45	3.4	1340	11	US-09-978-418-43	Sequence 43, Appl
581	46	3.5	3491	12	US-09-814-353-19345	Sequence 19345, A	C 654	45	3.4	1405	10	US-09-820-003A-1	Sequence 1, Appl
582	46	3.5	3521	9	US-09-860-868-1	Sequence 1, Appl	C 655	45	3.4	1414	14	US-10-106-698-2108	Sequence 2108, App
583	46	3.5	3521	14	US-10-163-435-12	Sequence 12, Appl	C 656	45	3.4	1436	14	US-09-764-864-272	Sequence 272, App
584	46	3.5	6410	9	US-09-922-217-1034	Sequence 1094, App	C 657	45	3.4	1492	14	US-10-180-375-29	Sequence 29, Appl
585	46	3.5	6410	13	US-10-025-380-1094	Sequence 1094, App	C 658	45	3.4	1577	14	US-10-059-909-13	Sequence 13, Appl
586	46	3.5	1223197	12	US-10-037-632-179264	Sequence 179264, A	C 659	45	3.4	1659	14	US-10-106-698-1996	Sequence 1996, App
587	46	3.5	1223197	13	US-10-027-632-179264	Sequence 179264, A	C 660	45	3.4	1659	14	US-09-796-692-667	Sequence 667, App
588	46	3.5	64	14	US-10-066-543-459	Sequence 459, App	C 661	45	3.4	1694	11	US-10-040-862-667	Sequence 667, App
589	46	3.4	128	14	US-10-066-543-1216	Sequence 1216, App	C 662	45	3.4	1711	9	US-09-925-301-157	Sequence 157, App
590	46	3.4	185	13	US-09-878-178-1615	Sequence 1615, App	C 663	45	3.4	1728	14	US-10-290-631-7	Sequence 7, Appl
591	46	3.4	185	13	US-10-046-935-1615	Sequence 1615, App	C 664	45	3.4	1767	10	US-09-764-846-107	Sequence 107, App
592	46	3.4	185	14	US-10-146-502-1615	Sequence 1615, App	C 665	45	3.4	1767	14	US-10-091-483-107	Sequence 107, App
593	46	3.4	202	9	US-09-925-299-573	Sequence 573, App	C 666	45	3.4	1779	11	US-09-892-877-108	Sequence 108, App
594	46	3.4	217	10	US-09-925-299-573	Sequence 573, App	C 667	45	3.4	1779	11	US-09-948-783-109	Sequence 109, App
595	46	3.4	217	10	US-09-878-574-12266	Sequence 12266, A	C 668	45	3.4	1797	12	US-09-790-039-1	Sequence 1, Appl
596	46	3.4	255	10	US-09-878-574-13064	Sequence 13064, A	C 669	45	3.4	1821	11	US-09-809-391-90	Sequence 90, Appl
597	46	3.4	274	14	US-10-106-698-948	Sequence 948, App	C 670	45	3.4				
598	46	3.4	276	10	US-09-878-574-14211	Sequence 14211, A	C 671	45	3.4				
599	46	3.4	302	9	US-09-925-299-710	Sequence 710, App	C 672	45	3.4				
600	46	3.4	302	11	US-09-925-299-710	Sequence 710, App	C 673	45	3.4				

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675	45	3.4	1821	12	US-09-882-171-90	Sequence 90, Appl	748	44	3.3	152	14	US-10-091-483-278	Sequence 278, App
676	45	3.4	1873	14	US-10-175-523-37	Sequence 37, Appl	749	44	3.3	153	10	US-09-933-797-793	Sequence 793, App
677	45	3.4	1877	13	US-10-007-399-2	Sequence 2, Appl	750	44	3.3	156	10	US-09-834-975-41	Sequence 41, Appl
678	45	3.4	2059	11	US-09-797-207-3	Sequence 3, Appl	751	44	3.3	158	9	US-09-764-869-1438	Sequence 1438, Ap
679	45	3.4	2108	9	US-09-930-213-290	Sequence 290, App	752	44	3.3	158	10	US-09-764-846-268	Sequence 268, App
680	45	3.4	2150	12	US-09-925-302-125	Sequence 125, App	753	44	3.3	158	10	US-09-764-846-275	Sequence 275, App
681	45	3.4	2381	9	US-09-909-20	Sequence 20, Appl	754	44	3.3	158	10	US-09-764-846-286	Sequence 286, App
682	45	3.4	2815	12	US-09-814-353-19687	Sequence 19687, A	755	44	3.3	158	10	US-09-764-846-338	Sequence 338, App
683	45	3.4	2938	12	US-09-198-846-10836	Sequence 10836, A	756	44	3.3	158	10	US-09-768-827-50	Sequence 50, Appl
684	45	3.4	3084	10	US-09-764-864-89	Sequence 89, Appl	757	44	3.3	158	11	US-09-764-891-7490	Sequence 7490, Ap
685	45	3.4	3393	9	US-09-732-224-1	Sequence 1, Appl	758	44	3.3	158	11	US-09-764-891-7705	Sequence 7705, Ap
686	45	3.4	3397	9	US-09-925-301-414	Sequence 414, App	759	44	3.3	158	14	US-10-031-483-268	Sequence 268, App
687	45	3.4	3465	9	US-09-729-674-81	Sequence 81, Appl	760	44	3.3	158	14	US-10-031-483-275	Sequence 275, App
688	45	3.4	4115	14	US-10-118-513A-1	Sequence 1, Appl	761	44	3.3	158	14	US-10-031-483-286	Sequence 286, App
689	45	3.4	4115	14	US-10-118-513A-7	Sequence 7, Appl	762	44	3.3	158	14	US-10-031-483-338	Sequence 338, App
690	45	3.4	4365	14	US-10-179-407-1	Sequence 1, Appl	763	44	3.3	158	14	US-10-091-504-1438	Sequence 1438, Ap
691	45	3.4	4524	12	US-09-287-218-34	Sequence 34, Appl	764	44	3.3	162	9	US-09-770-696-395	Sequence 395, App
692	45	3.4	5554	10	US-09-815-923-1	Sequence 1, Appl	765	44	3.3	162	14	US-10-066-543-1243	Sequence 1243, Ap
693	45	3.4	7034	14	US-10-118-513B-11	Sequence 11, Appl	766	44	3.3	165	10	US-09-998-598-992	Sequence 992, App
694	45	3.4	7536	12	US-10-311-455-1437	Sequence 1437, Ap	767	44	3.3	166	10	US-09-960-352-13009	Sequence 13009, A
695	45	3.4	8711	10	US-09-764-864-1783	Sequence 1783, Ap	768	44	3.3	174	11	US-09-925-299-750	Sequence 750, App
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699	44	3.3	71	10	US-09-983-965-131	Sequence 131, App	772	44	3.3	182	10	US-09-867-701-10159	Sequence 246, App
700	44	3.3	77	10	US-09-764-846-282	Sequence 282, App	773	44	3.3	187	9	US-09-770-696-246	Sequence 23, Appl
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702	44	3.3	80	13	US-10-046-722-15	Sequence 15, Appl	775	44	3.3	193	10	US-09-764-846-99	Sequence 1894, A
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704	44	3.3	81	14	US-10-228-070-15	Sequence 15, Appl	777	44	3.3	193	14	US-10-031-483-23	Sequence 99, Appl
705	44	3.3	86	10	US-10-066-543-1308	Sequence 1308, Ap	778	44	3.3	196	14	US-10-066-543-2605	Sequence 2605, Ap
706	44	3.3	86	10	US-09-768-827-39	Sequence 39, Appl	779	44	3.3	202	10	US-09-764-846-280	Sequence 280, App
707	44	3.3	89	9	US-09-925-301-774	Sequence 774, App	780	44	3.3	202	10	US-09-960-352-12507	Sequence 9114, Ap
708	44	3.3	89	10	US-09-919-580-374	Sequence 374, App	781	44	3.3	202	10	US-09-960-352-12507	Sequence 12507, A
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710	44	3.3	90	9	US-09-925-302-414	Sequence 414, App	783	44	3.3	203	10	US-09-960-352-1492	Sequence 1492, A
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714	44	3.3	103	10	US-09-924-035A-875	Sequence 875, App	787	44	3.3	211	10	US-09-867-701-2599	Sequence 5093, Ap
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716	44	3.3	105	14	US-10-228-070-23	Sequence 23, Appl	789	44	3.3	216	12	US-09-814-353-5000	Sequence 11292, A
717	44	3.3	105	14	US-10-066-543-872	Sequence 872, App	790	44	3.3	216	12	US-09-814-353-11292	Sequence 34, Appl
718	44	3.3	107	14	US-10-066-543-1787	Sequence 1787, Ap	791	44	3.3	216	13	US-10-040-916-34	Sequence 34, Appl
719	44	3.3	108	14	US-10-066-543-470	Sequence 470, App	792	44	3.3	216	14	US-10-016-249-34	Sequence 34, Appl
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724	44	3.3	115	9	US-09-770-696-747	Sequence 747, App	797	44	3.3	226	10	US-09-764-846-36	Sequence 36, Appl
725	44	3.3	115	10	US-09-924-035A-258	Sequence 258, App	798	44	3.3	226	14	US-10-091-483-36	Sequence 10334, A
726	44	3.3	116	14	US-10-066-543-761	Sequence 761, App	799	44	3.3	228	10	US-09-814-353-17588	Sequence 17588, A
727	44	3.3	118	10	US-09-960-352-8984	Sequence 8984, Ap	800	44	3.3	228	12	US-09-736-457-195	Sequence 195, App
728	44	3.3	120	8	US-08-463-404-44	Sequence 44, Appl	801	44	3.3	229	10	US-09-960-352-10224	Sequence 10224, A
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730	44	3.3	120	12	US-10-325-894-2	Sequence 2, Appl	803	44	3.3	230	14	US-10-106-698-1024	Sequence 1024, Ap
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732	44	3.3	122	14	US-10-066-543-807	Sequence 807, App	805	44	3.3	233	14	US-10-106-698-130	Sequence 130, App
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737	44	3.3	137	10	US-09-960-352-5686	Sequence 5686, Ap	810	44	3.3	239	10	US-09-960-352-11438	Sequence 11438, A
738	44	3.3	138	10	US-09-983-965-207	Sequence 207, App	811	44	3.3	239	10	US-09-960-352-13339	Sequence 13339, A
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C 821	44	3.3	241	10	US-09-960-352-7904	Sequence 7904, App	C 894	44	3.3	328	12	US-09-814-353-17578	Sequence 17578, A
C 822	44	3.3	241	10	US-09-960-352-12974	Sequence 12974, App	C 895	44	3.3	332	11	US-09-814-353-11438	Sequence 11438, A
C 823	44	3.3	241	12	US-09-814-353-8287	Sequence 8287, App	C 896	44	3.3	332	12	US-09-814-353-5594	Sequence 5594, App
C 824	44	3.3	242	10	US-09-960-352-9217	Sequence 9217, App	C 897	44	3.3	332	12	US-09-814-353-11881	Sequence 11881, App
C 825	44	3.3	242	14	US-10-98-846-9912	Sequence 9912, App	C 898	44	3.3	332	12	US-09-814-353-17583	Sequence 17583, A
C 826	44	3.3	248	12	US-09-814-353-15545	Sequence 15545, A	C 899	44	3.3	334	11	US-09-814-353-15303	Sequence 15303, A
C 827	44	3.3	255	12	US-09-814-353-1715	Sequence 715, App	C 900	44	3.3	335	10	US-09-814-353-453	Sequence 453, App
C 828	44	3.3	256	10	US-09-960-352-9413	Sequence 9413, App	C 901	44	3.3	336	12	US-09-814-353-4742	Sequence 4742, App
C 829	44	3.3	257	10	US-09-960-352-8890	Sequence 8890, App	C 902	44	3.3	336	12	US-09-814-353-11039	Sequence 11039, A
C 830	44	3.3	259	10	US-09-960-352-3453	Sequence 3453, App	C 903	44	3.3	337	9	US-09-770-791-889	Sequence 889, App
C 831	44	3.3	259	10	US-09-960-352-7233	Sequence 7233, App	C 904	44	3.3	337	10	US-09-960-352-6376	Sequence 6376, App
C 832	44	3.3	262	10	US-09-919-580-896	Sequence 896, App	C 905	44	3.3	344	10	US-09-960-352-13002	Sequence 13002, A
C 833	44	3.3	263	12	US-09-814-353-17766	Sequence 17766, A	C 906	44	3.3	346	12	US-09-814-353-17676	Sequence 17676, A
C 834	44	3.3	263	12	US-09-814-353-18283	Sequence 18283, A	C 907	44	3.3	347	10	US-09-960-352-1096	Sequence 1096, App
C 835	44	3.3	264	10	US-09-867-701-10185	Sequence 10185, A	C 908	44	3.3	347	10	US-09-960-352-3371	Sequence 3371, App
C 836	44	3.3	267	10	US-09-834-975-608	Sequence 608, App	C 909	44	3.3	349	9	US-09-770-791-712	Sequence 712, App
C 837	44	3.3	268	12	US-09-814-353-14902	Sequence 14902, A	C 910	44	3.3	349	12	US-09-814-353-4904	Sequence 4904, App
C 838	44	3.3	272	10	US-09-960-352-6986	Sequence 6986, App	C 911	44	3.3	349	12	US-09-814-353-11199	Sequence 11199, A
C 839	44	3.3	276	10	US-09-960-352-10131	Sequence 10131, A	C 912	44	3.3	349	12	US-09-814-353-18039	Sequence 18039, A
C 840	44	3.3	277	10	US-09-960-352-2296	Sequence 2296, App	C 913	44	3.3	350	9	US-09-770-791-701	Sequence 701, App
C 841	44	3.3	277	10	US-09-960-352-13673	Sequence 12673, A	C 914	44	3.3	350	12	US-09-960-352-11730	Sequence 11730, A
C 842	44	3.3	279	12	US-09-814-353-5914	Sequence 5914, App	C 915	44	3.3	350	12	US-09-814-353-5753	Sequence 5753, App
C 843	44	3.3	279	12	US-09-814-353-6306	Sequence 6306, App	C 916	44	3.3	350	12	US-09-814-353-17036	Sequence 17036, A
C 844	44	3.3	279	12	US-09-814-353-12195	Sequence 12195, A	C 917	44	3.3	350	12	US-09-814-353-18240	Sequence 18240, A
C 845	44	3.3	281	12	US-09-814-353-17584	Sequence 17584, A	C 918	44	3.3	351	9	US-09-770-791-691	Sequence 691, App
C 846	44	3.3	281	12	US-09-814-353-18204	Sequence 18204, A	C 919	44	3.3	351	12	US-09-814-353-4899	Sequence 4899, App
C 847	44	3.3	282	12	US-09-814-353-17457	Sequence 17457, A	C 920	44	3.3	351	12	US-09-814-353-11194	Sequence 11194, A
C 848	44	3.3	282	12	US-09-814-353-17553	Sequence 17553, A	C 921	44	3.3	351	12	US-09-814-353-17579	Sequence 17579, A
C 849	44	3.3	283	12	US-09-814-353-17553	Sequence 17553, A	C 922	44	3.3	355	10	US-09-960-352-2945	Sequence 2945, App
C 850	44	3.3	286	10	US-09-960-352-13342	Sequence 13342, A	C 923	44	3.3	355	10	US-09-960-352-14757	Sequence 14757, App
C 851	44	3.3	287	10	US-09-867-701-10057	Sequence 10057, A	C 924	44	3.3	358	12	US-09-814-353-6302	Sequence 6302, App
C 852	44	3.3	287	10	US-09-960-352-5888	Sequence 5888, App	C 925	44	3.3	358	12	US-09-814-353-12580	Sequence 12580, A
C 853	44	3.3	288	12	US-09-814-353-17819	Sequence 17819, A	C 926	44	3.3	358	12	US-09-814-353-18169	Sequence 18169, A
C 854	44	3.3	291	10	US-09-920-300A-192	Sequence 192, App	C 927	44	3.3	359	9	US-09-770-791-558	Sequence 558, App
C 855	44	3.3	291	10	US-09-960-352-1243	Sequence 1243, App	C 928	44	3.3	359	12	US-09-814-353-17359	Sequence 17359, A
C 856	44	3.3	291	10	US-09-960-352-13694	Sequence 13694, A	C 929	44	3.3	360	9	US-09-770-791-532	Sequence 532, App
C 857	44	3.3	291	13	US-10-099-928-132	Sequence 132, App	C 930	44	3.3	360	14	US-10-171-581-360	Sequence 360, App
C 858	44	3.3	291	13	US-10-033-528-132	Sequence 132, App	C 931	44	3.3	361	10	US-09-867-701-8566	Sequence 8566, App
C 859	44	3.3	294	12	US-09-814-353-5106	Sequence 5106, App	C 932	44	3.3	362	10	US-09-960-352-5390	Sequence 5390, App
C 860	44	3.3	294	12	US-09-814-353-11398	Sequence 11398, A	C 933	44	3.3	364	14	US-09-960-352-9419	Sequence 9419, App
C 861	44	3.3	295	14	US-09-764-846-33	Sequence 33, App	C 934	44	3.3	364	14	US-10-106-698-1442	Sequence 1442, App
C 862	44	3.3	295	14	US-10-091-483-33	Sequence 33, App	C 935	44	3.3	366	9	US-09-925-299-283	Sequence 283, App
C 863	44	3.3	296	12	US-09-814-353-5940	Sequence 5940, App	C 936	44	3.3	366	11	US-09-925-299-283	Sequence 283, App
C 864	44	3.3	296	12	US-09-814-353-12220	Sequence 12220, App	C 937	44	3.3	368	10	US-09-834-975-47	Sequence 47, App
C 865	44	3.3	299	10	US-09-867-701-10376	Sequence 10376, A	C 938	44	3.3	370	10	US-09-960-352-6169	Sequence 6169, App
C 866	44	3.3	300	10	US-09-960-352-6251	Sequence 6251, App	C 939	44	3.3	370	14	US-10-200-659-1	Sequence 1, App
C 867	44	3.3	300	12	US-09-814-353-5403	Sequence 5403, App	C 940	44	3.3	373	10	US-09-960-352-836	Sequence 836, App
C 868	44	3.3	300	12	US-09-814-353-11690	Sequence 11690, A	C 941	44	3.3	373	10	US-09-960-352-3655	Sequence 3655, App
C 869	44	3.3	304	10	US-09-764-846-109	Sequence 109, App	C 942	44	3.3	373	12	US-09-814-353-17141	Sequence 17141, A
C 870	44	3.3	304	14	US-10-091-483-109	Sequence 109, App	C 943	44	3.3	375	12	US-09-960-352-15014	Sequence 15014, A
C 871	44	3.3	305	12	US-09-814-353-5818	Sequence 5818, App	C 944	44	3.3	375	12	US-09-814-353-18474	Sequence 18474, A
C 872	44	3.3	305	12	US-09-814-353-12100	Sequence 12100, A	C 945	44	3.3	377	10	US-09-960-352-9425	Sequence 9425, App
C 873	44	3.3	307	10	US-09-764-846-54	Sequence 54, App	C 946	44	3.3	380	12	US-09-814-353-17491	Sequence 17491, A
C 874	44	3.3	307	14	US-10-091-483-54	Sequence 54, App	C 947	44	3.3	380	12	US-09-814-353-18006	Sequence 18006, A
C 875	44	3.3	308	10	US-09-960-352-7670	Sequence 7670, App	C 948	44	3.3	384	12	US-09-814-353-18604	Sequence 18604, A
C 876	44	3.3	310	10	US-09-867-701-10189	Sequence 10189, A	C 949	44	3.3	385	10	US-09-924-035A-848	Sequence 848, App
C 877	44	3.3	311	10	US-09-867-701-10189	Sequence 10189, A	C 950	44	3.3	385	12	US-09-814-353-5368	Sequence 5368, App
C 878	44	3.3	312	10	US-09-960-352-6315	Sequence 6315, App	C 951	44	3.3	385	12	US-09-814-353-11655	Sequence 11655, A
C 879	44	3.3	312	10	US-09-960-352-8414	Sequence 8414, App	C 952	44	3.3	385	12	US-09-814-353-19050	Sequence 19050, A
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C 881	44	3.3	314	10	US-09-764-846-126	Sequence 126, App	C 954	44	3.3	388	12	US-09-960-352-6680	Sequence 6680, App
C 882	44	3.3	314	14	US-10-091-483-126	Sequence 126, App	C 955	44	3.3	388	12	US-09-814-353-17525	Sequence 17525, A
C 883	44	3.3	316	12	US-09-814-353-16036	Sequence 16036, App	C 956	44	3.3	389	14	US-10-091-483-116	Sequence 116, App
C 884	44	3.3	317	10	US-09-960-352-2659	Sequence 2659, App	C 957	44	3.3	389	14	US-10-091-483-116	Sequence 116, App
C 885	44	3.3	318	10	US-09-960-352-5749	Sequence 5749, App	C 958	44	3.3	390	12	US-09-814-353-17808	Sequence 17808, A
C 886	44	3.3	318	10	US-09-960-352-5749	Sequence 5749, App	C 959	44	3.3	392	10	US-09-960-352-2634	Sequence 2634, App
C 887	44	3.3	318	12	US-09-814-353-6389	Sequence 6389, App	C 960	44	3.3	392	10	US-09-960-352-7679	Sequence 7679, App
C 888	44	3.3	318	12	US-09-814-353-12666	Sequence 12666, A	C 961	44	3.3	393	10	US-09-960-352-4582	Sequence 4582, App
C 889	44	3.3	323	10	US-09-960-352-10135	Sequence 10135, A	C 962	44	3.3	393	12	US-09-814-353-15254	Sequence 15254, A
C 890	44	3.3	325	10	US-09-764-846-30	Sequence 30, App	C 963	44	3.3	393	14	US-10-138-846-7182	Sequence 7182, App
C 891	44	3.3	325	10	US-09-960-352-8619	Sequence 8619, App	C 964	44	3.3	394	10	US-09-960-352-7714	Sequence 7714, App
C 892	44	3.3	325	14	US-10-091-483-30	Sequence 30, App	C 965	44	3.3	394	14	US-10-138-846-3918	Sequence 3918, App

us-10-024-806-1.oligo.rnpb

61	Qy	GTCA	GGCTCAAA	TACTCG	CGCTGC	ATCTC	CAAG	ACAC	TGCTCC	CTCTG	GGCTTCC	CGC	120
61	Db	GTCA	GGCTCAAA	TACTCG	CGCTGC	ATCTC	CAAA	AGCAC	TGCTCC	CTCTG	GGCTTCC	CGC	120
121	Qy	CTCT	CTTCC	GGCTCT	CGCTCC	CGAC	CGCCCT	CTAT	AGCC	CAAC	CGCGCC	GCAC	180
121	Db	CTCT	CTTCC	GGCTCT	CGCTCC	CGAC	CGCCCT	CTAT	AGCC	CAAC	CGCGCC	GCAC	180
181	Qy	GCAC	GACGAC	GAGTCT	CTCT	CCCC	GGCTCG	CGGTGG	AGCAG	CCGGGG	CGCGCG	CGCTTC	240
181	Db	GCAC	GACGAC	GAGTCT	CTCT	CCCC	GGCTCG	CGGTGG	AGCAG	CCGGGG	CGCGCG	CGCTTC	240
241	Qy	CGCG	GGGGTTC	GTAC	AGTTTGG	TGGAG	GGCGCG	CGCGCT	TCTCT	CCAC	GCCTG	CGGTCC	300
241	Db	CGCG	GGGGTTC	GTAC	AGTTTGG	TGGAG	GGCGCG	CGCGCT	TCTCT	CCAC	GCCTG	CGGTTC	300
301	Qy	GGCG	TGGGTTCT	TGGT	TGTGA	AAAC	CCAT	TGCTG	CTGT	TGA	CAAG	CAGTTG	360
301	Db	GGCG	TGGGTTCT	TGGT	TGTGA	AAAC	CCAT	TGCTG	CTGT	TGA	CAAG	CAGTTG	360
361	Qy	GATG	TACCA	AGCTG	GA	AGCT	CCAG	CTCT	GT	TGTAC	AGTGC	ATCTAG	420
361	Db	GATG	TACCA	AGCTG	GA	AGCT	CCAG	CTCT	GT	TGTAC	AGTGC	ATCTAG	420
421	Qy	AAGC	CAACT	CTCT	TAC	CCCTTC	GAAA	AGCAG	GATG	CAAG	GTTC	TG	480
421	Db	AAGC	CAACT	CTCT	TAC	CCCTTC	GAAA	AGCAG	GATG	CAAG	GTTC	TG	480
481	Qy	TCCT	CGAA	AGCT	CTCA	AGG	GTCT	CCAA	AGAG	TTG	AG	CATCTG	540
481	Db	TCCT	CGAA	AGGCT	CTCA	AGG	GTCT	CCAA	AGAG	TTG	AG	CATCTG	540
541	Qy	ACCT	TCGG	AGAG	ATGTTT	CAAA	AGAG	CTGAT	GT	TAG	AGTCTAT	TATGA	600
541	Db	ACCT	TCGG	AGAG	ATGTTT	CAAA	AGAG	CTGAT	GT	TAG	AGTCTAT	TATGA	600

RESULTS

QY	720	TTGATGAGGATGAGAGAAATCTCAGTGGCGAAGCTAAATTGATCTGAATCTTACTTGGCGTC	720
Db	720	TTGATGAGGATGAGAGAAATCTCAGTGGCGAAGCTAAATTGATCTGAATCTTACTTGGCGTC	720
QY	760	TTCTTTTGTCACAGCGCTGCACAAAAGTAATGATGAAAAGACAGAGAGGAAAATTTATC	760
Db	760	TTCTTTTGTCACAGCGCTGCACAAAAGTAATGATGAAAAGACAGAGAGGAAAATTTATC	760
QY	840	AACATTCGATCTGTAGTTGGTCTTACTGGCAATGTGGCCMAAGCTTAATTTAGCGCGACCC	840
Db	840	AACATTCGATCTGTAGTTGGTCTTACTGGCAATGTGGCCMAAGCTTAATTTAGCGCGACCC	840
QY	900	AAGCTCGAGTGATTTGGTTTTCAAAAACAGTTGCCAGCGGAGTATGCAAGCAGAGAAATATC	900
Db	900	AAGCTCGAGTGATTTGGTTTTCAAAAACAGTTGCCAGCGGAGTATGCAAGCAGAGAAATATC	900
QY	960	AATCTGAATGCTATTGCACCGAGGTTCTATTGCATCTGATATGACTGCCGAACTTGGAGAA	960
Db	960	AATCTGAATGCTATTGCACCGAGGTTCTATTGCATCTGATATGACTGCCGAACTTGGAGAA	960
QY	1020	GAGCTTGAGAGAAAATCTTTGTCAACCAATTCGGTTAGGGAGATATGGCCAAACCAAGAGAA	1020
Db	1020	GAGCTTGAGAGAAAATCTTTGTCAACCAATTCGGTTAGGGAGATATGGCCAAACCAAGAGAA	1020

QY	1022	GTTCAGGGTTGGTCGAGTTCCTTGGCCCTTACC	CCGCGAGCTGAGCTATATGACTTGGACAG	1080
Db	1021	GTTCAGGGTTGGTCGAGTTCCTTGGCCCTTACC	CCGCGAGCTGAGCTATATGACTTGGACAG	1080
QY	1081	GTGCTTCAATGTACGGAGGATGGTAATGTGAAGATTTGAGTACCTTGA	TGCACCTTCTA	1140
Db	1081	GTGCTTCAATGTACGGAGGATGGTAATGTGAAGATTTGAGTACCTTGA	TGCACCTTCTA	1140

;; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
;; TITLE OF INVENTION: Stress Response

;; FILE REFERENCE: BSI357 US NA

;; CURRENT APPLICATION NUMBER: US/10/078,929

;; CURRENT FILING DATE: 2002-02-19

;; PRIOR APPLICATION NUMBER: 09/566,394

;; PRIOR FILING DATE: 2000-05-05

;; PRIOR APPLICATION NUMBER: 60/133038

;; PRIOR FILING DATE: 1999-05-07

;; PRIOR APPLICATION NUMBER: 60/133042

;; PRIOR FILING DATE: 1999-05-07

;; PRIOR APPLICATION NUMBER: 60/133427

;; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 60/133437

;; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 60/133428

;; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 60/133438

;; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 60/133436

;; PRIOR FILING DATE: 1999-05-11

;; PRIOR APPLICATION NUMBER: 60/137667

;; PRIOR FILING DATE: 1999-06-04

;; NUMBER OF SEQ ID NOS: 208

;; SOFTWARE: Microsoft Office 97

;; SEQ ID NO 89

;; LENGTH: 939

;; TYPE: DNA

;; ORGANISM: Glycine max

;; US-10-078-929-89

Query Match 3.5%; Score 47; DB 13; Length 939;

Best Local Similarity 100.0%; Pred. No. 3.2e-12;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA 1326

DB 886 GTGTAAAAA 932

RESULT 6

US-09-984-245-111

Sequence 111, Application US/09984245

Patent No. US20020165374A1

GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 87 Human Secreted Proteins

FILE REFERENCE: P2004P1

CURRENT APPLICATION NUMBER: US/09/984,245

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: 09/154,707

PRIOR FILING DATE: 1998-09-17

PRIOR APPLICATION NUMBER: PCT/US98/05311

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: US 60/041,277

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/042,344

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/041,276

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/041,281

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/048,094

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048,350

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048,188

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048,135

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/050,937

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/048,187

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,099

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,352

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,186

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,069

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,095

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,131

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,096

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,355

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,160

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,351

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/048,154

;; PRIOR FILING DATE: 1997-05-30

;; PRIOR APPLICATION NUMBER: US 60/054,804

;; PRIOR FILING DATE: 1997-08-05

;; PRIOR APPLICATION NUMBER: US 60/056,370

;; PRIOR FILING DATE: 1997-08-19

;; PRIOR APPLICATION NUMBER: US 60/060,862

;; PRIOR FILING DATE: 1997-10-02

;; NUMBER OF SEQ ID NOS: 343

;; SOFTWARE: Patentin ver. 2.0

;; SEQ ID NO 111

;; LENGTH: 1015

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; NAME/KEY: misc feature

;; LOCATION: (1013)

;; OTHER INFORMATION: n equals a,t,g, or c

;; US-09-984-245-111

Query Match 3.5%; Score 47; DB 10; Length 1015;

Best Local Similarity 100.0%; Pred. No. 3.2e-12;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA 1326

DB 947 GTGTAAAAA 993

RESULT 7

US-09-966-262-111

Sequence 111, Application US/09966262

Publication No. US20030050461A1

GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 87 Human Secreted Proteins

FILE REFERENCE: P2004P1

CURRENT APPLICATION NUMBER: US/09/966,262

CURRENT FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: US 09/154,707

PRIOR FILING DATE: 1998-09-17

PRIOR APPLICATION NUMBER: PCT/US98/05311

PRIOR FILING DATE: 1998-03-19

PRIOR APPLICATION NUMBER: US 60/041,277

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/042,344

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/041,276

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/041,281

PRIOR FILING DATE: 1997-03-21

PRIOR APPLICATION NUMBER: US 60/048,094

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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
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; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 1015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1014)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-966-262-111

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Query Match      3.5%; Score 47; DB 11; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326
DB 947 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 993

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RESULT 8
US-09-983-966-111
; Sequence 111, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311

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; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
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; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 1015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1014)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-983-966-111

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Query Match      3.5%; Score 47; DB 11; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1280 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326
DB 947 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 993

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RESULT 9
US-10-143-090-111
; Sequence 111, Application US/10143090

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; Publication No. US20030069406A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/10/143,090
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 1015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1014)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-143-090-111

Query Match      3.5%; Score 47; DB 14; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326
Db 947 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 993

RESULT 10
US-10-012-542-36
; Sequence 36, Application US/10012542
; Publication No. US2003004851A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (63)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1201)
; OTHER INFORMATION: n equals a,t,g, or c

US-10-012-542-36
Query Match      3.5%; Score 47; DB 14; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326
Db 947 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 993

US-10-012-542-36
Query Match      3.5%; Score 47; DB 14; Length 1201;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326
Db 1131 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1177

RESULT 11
US-09-764-853-227
; Sequence 227, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P2006
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: n equals a,t,g, or c

US-09-764-853-227
Query Match      3.5%; Score 47; DB 9; Length 1371;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1326
Db 1276 GTGTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1322

RESULT 12
US-09-925-301-584
; Sequence 584, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P2106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 584
; LENGTH: 2968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (454)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1437)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2961)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2964)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-301-584
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Query Match 3.5%; Score 47; DB 9; Length 2968;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 GTGTAAAAA..... 1326
Db 2887 GTGTAAAAA..... 2933

RESULT 13
US-10-106-698-1500
; Sequence 1500, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: P00581
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1500
; LENGTH: 2968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2961)..(2961)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (2964)..(2964)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1500

Query Match 3.5%; Score 47; DB 14; Length 2968;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 GTGTAAAAA..... 1326
Db 2887 GTGTAAAAA..... 2933

RESULT 14
US-10-027-000-1
; Sequence 1, Application US/10027000
; Publication No. US20030119006A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Goedegebuur, Frits
; APPLICANT: Ward, Michael
; APPLICANT: Yao, Jian
; TITLE OF INVENTION: BGL4 Beta-Glucosidase and Nucleic Acids
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: GC696
; CURRENT APPLICATION NUMBER: US/10/027,000
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Trichoderma reesei
US-10-027-000-1

Query Match 3.5%; Score 47; DB 14; Length 2976;

Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 GTGTAAAAA..... 1326
Db 2918 GTGTAAAAA..... 2964

RESULT 15
US-10-102-524-963
; Sequence 963, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 963
; LENGTH: 269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-524-963

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Best Local Similarity 100.0%; Pred. No. 9.6e-12;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1281 TGTAAAAA..... 1326
Db 158 TGTAAAAA..... 203

Search completed: November 7, 2003, 21:02:16
Job time : 465 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 16:57:25 ; Search time 3088 Seconds
(without alignments)
10436.443 Million cell updates/sec

Title: US-10-024-806-1
Perfect score: 1326
Sequence: 1 gcgcggagcttccaaagccc.....aaaaaaaaaaaaaaaaaaaa 1326

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

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8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_eston:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

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24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	80	47	3.5	161	12	BI396078	94904A08	153	47	3.5	349	10	BE586652
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	82	47	3.5	169	13	BQ080880	san1ld09	155	47	3.5	361	13	BUT74086
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	86	47	3.5	186	9	AL7062908	IL3-UT011	159	47	3.5	370	14	CB048769
	87	47	3.5	186	9	AL7062908	IL3-UT011	158	47	3.5	372	9	AW783911
	88	47	3.5	186	9	AL7062908	IL3-UT011	158	47	3.5	372	14	CA500114
	89	47	3.5	189	14	CB059818	ca93a09.x	159	47	3.5	381	10	BG383956
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	91	47	3.5	194	9	AW156558	se28f09.y	160	47	3.5	383	14	WI0540
	92	47	3.5	197	12	BG981996	CG100687	161	47	3.5	384	13	BQ1919834
	93	47	3.5	197	13	BUT555823	CG100687	162	47	3.5	385	9	AF082705
	94	47	3.5	198	9	AI281825	BU555823	163	47	3.5	385	9	AF082705
	95	47	3.5	198	12	BG980725	BU555823	164	47	3.5	387	9	AA830596
	96	47	3.5	198	14	CA455506	AGENCOURT	165	47	3.5	387	13	BY672161
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	101	47	3.5	207	14	CB976392	AGENCOURT	170	47	3.5	392	10	BE500028
	102	47	3.5	210	9	AL501426	AGENCOURT	171	47	3.5	400	14	CD107086
	103	47	3.5	211	9	AL502061	AGENCOURT	172	47	3.5	400	14	CD107086
	104	47	3.5	216	9	AA241178	AGENCOURT	173	47	3.5	402	14	CB522861
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	107	47	3.5	236	14	CA466679	AGENCOURT	176	47	3.5	405	9	AA253856
	108	47	3.5	241	12	HSM066880	AGENCOURT	177	47	3.5	410	14	CA518188
	109	47	3.5	241	2	HSM063202	AGENCOURT	178	47	3.5	410	14	CA518188
	110	47	3.5	245	10	BF151711	AGENCOURT	179	47	3.5	412	9	AL681614
	111	47	3.5	256	14	CA453796	AGENCOURT	180	47	3.5	421	9	AA184454
	112	47	3.5	260	9	AO076173	AGENCOURT	181	47	3.5	429	9	AA184454
	113	47	3.5	261	14	CA993646	AGENCOURT	182	47	3.5	431	13	BQ943098
	114	47	3.5	263	12	BI268712	AGENCOURT	183	47	3.5	439	12	BM690248
	115	47	3.5	266	14	CD209279	AGENCOURT	184	47	3.5	442	14	CD393756
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	117	47	3.5	272	14	CA754309	AGENCOURT	186	47	3.5	445	10	BE685292
	118	47	3.5	276	14	CB824010	AGENCOURT	187	47	3.5	450	14	CB541125
	119	47	3.5	278	13	BU533303	AGENCOURT	188	47	3.5	451	12	BI680793
	120	47	3.5	279	9	AA268052	AGENCOURT	189	47	3.5	453	9	AW632028
	121	47	3.5	283	10	BE752983	AGENCOURT	190	47	3.5	455	9	AW632028
	122	47	3.5	286	9	AI544870	AGENCOURT	191	47	3.5	457	13	BQ619218
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	130	47	3.5	300	9	AW472906	AGENCOURT	199	47	3.5	490	12	BI490819
	131	47	3.5	302	9	AO057109	AGENCOURT	200	47	3.5	490	14	CD447235
	132	47	3.5	303	9	AW156713	AGENCOURT	201	47	3.5	499	9	AI352363
	133	47	3.5	310	14	CB215986	AGENCOURT	202	47	3.5	502	14	CB049560
	134	47	3.5	312	13	BU773426	AGENCOURT	203	47	3.5	515	13	BQ548179
	135	47	3.5	315	10	BF199089	AGENCOURT	204	47	3.5	517	13	BQ527685
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	138	47	3.5	325	14	CB679722	AGENCOURT	207	47	3.5	535	13	BQ748454
	139	47	3.5	325	14	CB679722	AGENCOURT	208	47	3.5	540	11	BC038096
	140	47	3.5	326	10	BF067626	AGENCOURT	209	47	3.5	540	13	BQ179254
	141	47	3.5	328	9	AI172944	AGENCOURT	210	47	3.5	543	9	AV693602
	142	47	3.5	329	12	BM063269	AGENCOURT	211	47	3.5	545	9	AA898405
	143	47	3.5	329	12	BM063269	AGENCOURT	212	47	3.5	546	9	AA898405
	144	47	3.5	330	9	AI1812107	AGENCOURT	213	47	3.5	547	11	AY105694
	145	47	3.5	331	14	CB722623	AGENCOURT	214	47	3.5	557	9	AW055888
	146	47	3.5	333	14	CA779308	AGENCOURT	215	47	3.5	578	12	BM941162
	147	47	3.5	337	13	BU529438	AGENCOURT	216	47	3.5	581	14	CB196287
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		47	3.5					223	47	3.5	644	14	CD400785

C 224	47	3.5	652	13	BQ401053	NISC mp12	297	46	3.5	119	14	CA779629	CA779629
225	47	3.5	656	12	BI689464	603315324	298	46	3.5	120	12	BQ335942	BQ335942
226	47	3.5	663	9	AV723809	AV723809	299	46	3.5	120	12	BM889234	BM889234
227	47	3.5	671	9	AU092861	AU092861	300	46	3.5	120	14	CB857902	CB857902
C 228	47	3.5	683	9	AI446536	tj05b10.x	301	46	3.5	121	9	AW059474	AW059474
C 229	47	3.5	691	9	AL040394	DFZP434A	302	46	3.5	121	12	BM014835	BM014835
230	47	3.5	692	9	AU082650	AU082650	303	46	3.5	121	12	BM014835	BM014835
231	47	3.5	704	9	AV704051	AV704051	304	46	3.5	122	9	AW156369	AW156369
232	47	3.5	708	9	AU092879	AU092879	305	46	3.5	123	12	BI500834	BI500834
233	47	3.5	769	13	BQ534360	BQ534360	306	46	3.5	123	13	BQ298861	BQ298861
234	47	3.5	771	13	BQ556340	BQ556340	307	46	3.5	126	12	BI494423	BI494423
235	47	3.5	781	9	AV755884	AV755884	308	46	3.5	126	12	BM553760	BM553760
C 236	47	3.5	785	11	AV109066	AV109066	C 309	46	3.5	129	9	AL891816	AL891816
237	47	3.5	798	12	BI521970	603081178	310	46	3.5	129	10	BG554133	BG554133
238	47	3.5	805	14	CB317231	CB317231	C 311	46	3.5	129	10	BE345151	BE345151
239	47	3.5	815	13	BQ530863	BQ530863	312	46	3.5	130	2	HS0005765	HS0005765
240	47	3.5	835	13	BQ844198	BQ844198	313	46	3.5	130	12	BI495506	BI495506
241	47	3.5	848	14	CD102590	CD102590	314	46	3.5	131	14	CA820409	CA820409
242	47	3.5	849	10	BF792928	BF792928	315	46	3.5	133	9	AA473421	AA473421
243	47	3.5	864	13	EX384297	EX384297	316	46	3.5	135	14	CB345986	CB345986
244	47	3.5	869	11	AY107466	AY107466	317	46	3.5	135	14	CD521161	CD521161
245	47	3.5	873	13	BQ589694	BQ589694	C 318	46	3.5	136	12	BG952913	BG952913
246	47	3.5	894	13	BQ842087	BQ842087	C 319	46	3.5	138	9	AI250282	AI250282
247	47	3.5	902	13	EX452314	EX452314	C 320	46	3.5	138	9	AW430029	AW430029
C 248	47	3.5	909	10	BF204118	BF204118	321	46	3.5	138	13	BQ802750	BQ802750
249	47	3.5	913	13	BQ157923	BQ157923	322	46	3.5	138	14	CD018855	CD018855
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C 253	47	3.5	982	12	BI519101	BI519101	326	46	3.5	142	9	AA138195	AA138195
C 254	47	3.5	1005	13	EX431381	EX431381	327	46	3.5	142	14	CB410602	CB410602
C 255	47	3.5	1015	10	BF787276	BF787276	C 328	46	3.5	142	14	CD400059	CD400059
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C 257	47	3.5	1064	12	BM458007	BM458007	330	46	3.5	144	9	AA624174	AA624174
C 258	47	3.5	1082	14	CD050637	CD050637	331	46	3.5	144	13	BQ851107	BQ851107
C 259	47	3.5	1098	13	BQ393072	BQ393072	332	46	3.5	145	14	AV747571	AV747571
C 260	47	3.5	1100	11	AF111845	AF111845	333	46	3.5	145	12	BM873757	BM873757
C 261	47	3.5	1101	13	BQ418108	BQ418108	334	46	3.5	148	13	BQ766353	BQ766353
C 262	47	3.5	1106	13	BQ304113	BQ304113	335	46	3.5	148	13	AA120297	AA120297
C 263	47	3.5	1120	10	BQ389186	BQ389186	336	46	3.5	149	12	BQ483326	BQ483326
C 264	47	3.5	1121	10	BE964617	BE964617	337	46	3.5	150	12	AW45752	AW45752
C 265	47	3.5	1169	12	BM537774	BM537774	338	46	3.5	150	10	BQ945732	BQ945732
C 266	47	3.5	1198	14	CB573667	CB573667	C 339	46	3.5	150	12	BI001702	BI001702
C 267	47	3.5	1272	13	EX410576	EX410576	340	46	3.5	150	13	BQ618442	BQ618442
C 268	47	3.5	1353	11	AY106460	AY106460	341	46	3.5	150	14	CA500472	CA500472
C 269	47	3.5	1567	10	BE966259	BE966259	342	46	3.5	150	14	CB410005	CB410005
C 270	47	3.5	1736	12	BI519160	BI519160	343	46	3.5	152	9	AI287386	AI287386
C 271	47	3.5	1919	11	AY106207	AY106207	344	46	3.5	152	11	AK085205	AK085205
C 272	47	3.5	1966	10	BE747901	BE747901	345	46	3.5	152	13	BQ799802	BQ799802
273	47	3.5	2070	11	BC039012	BC039012	346	46	3.5	152	13	BU565047	BU565047
C 274	47	3.5	3646	11	BC036448	BC036448	347	46	3.5	154	9	AI439062	AI439062
C 275	46	3.5	61	9	AA743941	AA743941	348	46	3.5	154	9	AI499847	AI499847
C 276	46	3.5	66	9	AI872315	AI872315	349	46	3.5	154	9	AL036705	AL036705
C 277	46	3.5	82	9	AA548552	AA548552	C 350	46	3.5	154	10	BG456624	BG456624
C 278	46	3.5	84	14	T25665	T25665	351	46	3.5	156	12	BI037521	BI037521
C 279	46	3.5	88	10	BG664440	BG664440	352	46	3.5	157	12	BI781590	BI781590
C 280	46	3.5	88	10	BE325908	BE325908	353	46	3.5	157	12	BM516837	BM516837
C 281	46	3.5	97	9	AI077701	AI077701	354	46	3.5	158	14	BG956228	BG956228
C 282	46	3.5	97	10	BF120069	BF120069	355	46	3.5	158	14	CD521126	CD521126
C 283	46	3.5	100	10	BE724073	BE724073	C 356	46	3.5	159	9	AL716080	AL716080
C 284	46	3.5	100	12	BM863232	BM863232	C 357	46	3.5	161	12	BM307404	BM307404
C 285	46	3.5	100	14	CB083698	CB083698	358	46	3.5	162	13	BU844048	BU844048
C 286	46	3.5	104	14	CB409569	CB409569	359	46	3.5	163	14	CA780240	CA780240
C 287	46	3.5	105	12	BQ368060	BQ368060	360	46	3.5	164	9	AA185872	AA185872
C 288	46	3.5	107	9	AI273919	AI273919	361	46	3.5	164	10	BM560616	BM560616
C 289	46	3.5	112	14	CD401757	CD401757	C 362	46	3.5	165	9	AA159060	AA159060
C 290	46	3.5	113	9	AI678623	AI678623	363	46	3.5	165	9	AA159060	AA159060
C 291	46	3.5	113	12	BQ998183	BQ998183	364	46	3.5	165	14	BU587582	BU587582
C 292	46	3.5	113	13	BQ265348	BQ265348	365	46	3.5	165	14	CB566929	CB566929
C 293	46	3.5	113	13	BU188149	BU188149	366	46	3.5	166	9	AI288285	AI288285
C 294	46	3.5	114	14	CD407086	CD407086	367	46	3.5	166	9	AL716065	AL716065
C 295	46	3.5	115	9	AW075382	AW075382	368	46	3.5	166	9	AW359147	AW359147
C 296	46	3.5	118	14	CA337161	CA337161	369	46	3.5	167	9	AU261802	AU261802
C 297	46	3.5	118	14	CA337161	CA337161	370	46	3.5	167	9	AU261802	AU261802
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C 299	46	3.5	118	14	CA337161	CA337161	372	46	3.5	167	9	AU261802	AU261802
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C 302	46	3.5	118	14	CA337161	CA337161	375	46	3.5	167	9	AU261802	AU261802
C 303	46	3.5	118	14	CA337161	CA337161	376	46	3.5	167	9	AU261802	AU261802
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C 307	46	3.5	118	14	CA337161	CA337161	380	46	3.5	167	9	AU261802	AU261802
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C 309	46	3.5	118	14	CA337161	CA337161	382	46	3.5	167	9	AU261802	AU261802
C 310	46	3.5	118	14	CA337161	CA337161	383	46	3.5	167	9	AU261802	AU261802
C 311	46	3.5	118	14	CA337161	CA337161	384	46	3.5	167	9	AU261802	AU261802
C 312	46	3.5	118	14	CA337161	CA337161	385	46	3.5	167	9	AU261802	AU261802
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C 371	46	3.5	168	14	CA342847	NC
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C 373	46	3.5	169	10	BE891834	601434280
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C 375	46	3.5	173	12	BI145661	602909801
C 376	46	3.5	173	12	BI738659	603358879
C 377	46	3.5	173	14	CA819116	saug69c08.r
C 378	46	3.5	174	14	CB409269	NCSC.nc04
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C 387	46	3.5	180	12	BM030226	488800 MA
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C 392	46	3.5	183	9	AL696076	DKFZP686A
C 393	46	3.5	184	9	AI652664	wb30d02.x
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C 400	46	3.5	185	12	BI714719	ic04h09.y
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C 407	46	3.5	186	13	BU944985	AGENCOURT
C 408	46	3.5	187	10	BF970768	602273782
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C 410	46	3.5	187	14	CA337036	NISC lv08
C 411	46	3.5	188	9	AW033158	AU031158
C 412	46	3.5	189	9	AL707832	DKFZP686L
C 413	46	3.5	189	10	BF527014	602070296
C 414	46	3.5	189	12	BI652330	603299790
C 415	46	3.5	190	10	BG631028	cc-esf1cL
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C 427	46	3.5	192	9	AA388573	vc95h05.r
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C 434	46	3.5	194	12	BI782405	kh25c03.y
C 435	46	3.5	194	12	BM092222	eah09g02.
C 436	46	3.5	194	12	BM093888	sa22d10.
C 437	46	3.5	194	14	CB857623	NISC.na08
C 438	46	3.5	194	14	CD387849	AGENCOURT
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C 442	46	3.5	197	9	AW133441	se19a07.y
C 443	46	3.5	197	10	BF595660	
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C 451	46	3.5	199	10	BE807222	
C 452	46	3.5	199	12	BM896894	
C 453	46	3.5	200	13	BQ288161	
C 454	46	3.5	200	13	BU565550	
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C 457	46	3.5	201	9	AW756874	
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C 467	46	3.5	208	9	AW051524	
C 468	46	3.5	208	9	AW099490	
C 469	46	3.5	208	9	AW311554	
C 470	46	3.5	208	10	BG155209	
C 471	46	3.5	208	12	BG991160	
C 472	46	3.5	208	12	BM158603	
C 473	46	3.5	209	14	CA807128	
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C 481	46	3.5	213	12	BI345522	
C 482	46	3.5	214	9	AA217651	
C 483	46	3.5	214	9	AW099547	
C 484	46	3.5	214	9	AW065534	
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C 516	46	3.5	224	9	AI582910	AI582910 ts07e04.x	589	46	3.5	250	9	AU262843	AU262843
517	46	3.5	224	9	AI609967	AI609967 tt78b07.x	590	46	3.5	250	14	CA715111	CA715111 wdk3c.pk0
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520	46	3.5	225	10	BE133484	BE133484 ug33f11.y	593	46	3.5	252	10	BG237440	BG237440 sbl13f08.
C 521	46	3.5	225	13	BQ586919	BQ586919 S013305-0	C 594	46	3.5	252	12	BG944802	BG944802 ax55405.x
522	46	3.5	226	9	AW119776	AW119776 sds2d05.y	595	46	3.5	252	13	BQ785407	BQ785407 seq77c10.x
523	46	3.5	228	9	AU097528	AU097528 AU097528	596	46	3.5	253	9	AA596935	AA596935 vol4h02.r
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C 525	46	3.5	228	14	CD391503	CD391503 GM CK1040	C 598	46	3.5	254	14	H24048	H24048 ym54b08.sl
526	46	3.5	229	9	AL697945	AL697945 DKFZp686F	599	46	3.5	255	9	AW395275	AW395275 sh46a12.y
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C 528	46	3.5	230	9	AI811812	AI811812 tw32d10.x	C 601	46	3.5	256	14	CB857612	CB857612 NISC na08
529	46	3.5	230	9	AA218408	AA218408 mw59f11.x	602	46	3.5	257	10	BE667416	BE667416 151768.MA
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531	46	3.5	230	14	CB932435	CB932435 r189901.y	604	46	3.5	258	12	BM033740	BM033740 kb67a04.y
532	46	3.5	231	9	AA250449	AA250449 mz59d06.r	605	46	3.5	258	13	BU960464	BU960464 AGENCOURT
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534	46	3.5	231	10	BE749895	BE749895 200970.MA	607	46	3.5	258	14	CB944780	CB944780 AGENCOURT
535	46	3.5	231	13	BU851863	BU851863 AGENCOURT	608	46	3.5	259	12	BM988329	BM988329 ph63e08.y
C 536	46	3.5	232	9	AW081349	AW081349 xc41b07.x	C 609	46	3.5	259	13	BQ107860	BQ107860 NXLV101.E
537	46	3.5	232	14	CB278228	CB278228 EST1131.Z	610	46	3.5	261	13	BA76487	BA76487 DKFZp686G
538	46	3.5	233	9	AJ499187	AJ499187 AJ499187	C 611	46	3.5	262	9	AI590918	AI590918 tw89a06.x
539	46	3.5	233	10	BG452647	BG452647 NF079B01L	C 612	46	3.5	263	10	BG610382	BG610382 tw25c09.x
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542	46	3.5	234	10	BE807978	BE807978 213073.MA	615	46	3.5	264	12	BM495162	BM495162 lpc3gr1.8
543	46	3.5	234	13	BU709882	BU709882 fs45c05.y	616	46	3.5	265	9	AI681101	AI681101 AL681101-
544	46	3.5	235	9	AA561629	AA561629 v101g06.r	C 617	46	3.5	265	10	BF753027	BF753027 RC3-BN042
C 545	46	3.5	235	10	BE248003	BE248003 NF001F10D	C 618	46	3.5	266	9	AI682741	AI682741 wc65f02.x
546	46	3.5	235	12	BJ369197	BJ369197 BJ369197	619	46	3.5	266	9	AW161402	AW161402 au81d02.y
547	46	3.5	235	12	BM569884	BM569884 ih99c09.y	620	46	3.5	266	9	AW640206	AW640206 bl92e04.w
548	46	3.5	235	12	BM97553	BM97553 ph42g11.y	621	46	3.5	266	12	BM897105	BM897105 ph56g02.y
549	46	3.5	235	14	CB410344	CB410344 NISC nc11	622	46	3.5	266	13	BQ8990702	BQ8990702 AGENCOURT
C 550	46	3.5	236	12	BM988221	BM988221 ph61h02.y	C 624	46	3.5	267	13	BU531585	BU531585 AGENCOURT
551	46	3.5	236	14	CB854122	CB854122 UI-CF-DUL	625	46	3.5	267	14	CA807570	CA807570 ESG018C.E
552	46	3.5	237	9	AI345557	AI345557 tb83c12.x	626	46	3.5	268	12	BG950495	BG950495 PMO-CT070
553	46	3.5	237	9	AI395217	AI395217 MA002647.	C 627	46	3.5	268	12	BI502129	BI502129 kt85g01.y
C 554	46	3.5	237	12	BI003482	BI003482 MR3-HN012	C 628	46	3.5	269	9	AA183003	AA183003 mt78b04.r
555	46	3.5	238	9	AI435645	AI435645 th47h07.x	629	46	3.5	269	10	BG337222	BG337222 saa38d09.
C 556	46	3.5	238	9	AL884619	AL884619 AL884619	630	46	3.5	269	13	BQ392439	BQ392439 NISC mq24
557	46	3.5	238	13	BQ803686	BQ803686 WHE2840.E	C 631	46	3.5	269	13	BQ392439	BQ392439 K-EST0187
558	46	3.5	239	9	AI696321	AI696321 tw59c09.x	C 632	46	3.5	269	14	CA135367	CA135367 K-EST0187
C 559	46	3.5	239	12	BI337445	BI337445 360808.MA	C 633	46	3.5	270	9	AA268920	AA268920 va44g09.r
560	46	3.5	239	12	BM964556	BM964556 lpc3gr2.1	634	46	3.5	270	14	CA336177	CA336177 NISC lu09
561	46	3.5	240	10	BE757773	BE757773 212305.MA	C 635	46	3.5	271	9	AA713578	AA713578 nv68b06.s
562	46	3.5	241	9	AL117864	AL117864 p8730b11	636	46	3.5	271	12	BM270601	BM270601 sak15c05.
563	46	3.5	241	9	AW482910	AW482910 48518.MAR	C 637	46	3.5	271	14	CA819063	CA819063 sau68d07.
C 564	46	3.5	241	14	CD402210	CD402210 GM CK2482	638	46	3.5	272	9	AW827193	AW827193 xn08h08.y
565	46	3.5	241	9	AI559412	AI559412 t333d03.x	639	46	3.5	272	13	BQ930150	BQ930150 AGENCOURT
C 566	46	3.5	242	9	AJ541679	AJ541679 AJ541679	640	46	3.5	273	10	BG222103	BG222103 naj39e10.
567	46	3.5	242	9	AU095094	AU095094 AU095094	641	46	3.5	274	9	AI634467	AI634467 ty98h01.x
568	46	3.5	242	9	AW396620	AW396620 sg80d06.y	C 642	46	3.5	274	14	CD418263	CD418263 Gm CK9309
569	46	3.5	242	14	CA342649	CA342649 672587.NC	643	46	3.5	275	9	AU029507	AU029507 AU029507
C 570	46	3.5	243	9	AA227497	AA227497 zrl8f04.s	644	46	3.5	275	10	BE198796	BE198796 ug82f08.y
571	46	3.5	243	12	BM367026	BM367026 NXLV 043	645	46	3.5	275	12	BI962746	BI962746 ie54b03.y
572	46	3.5	243	14	CA790210	CA790210 AGENCOURT	C 646	46	3.5	276	9	AI274484	AI274484 qv61d10.x
573	46	3.5	243	13	BY922110	BY922110 NISC mq23	647	46	3.5	276	10	BG654228	BG654228 sad53d08.
C 574	46	3.5	244	13	CA902130	CA902130 NISC mq23	648	46	3.5	277	10	BE751167	BE751167 203044.MA
575	46	3.5	245	9	AU092510	AU092510 AU092510	C 649	46	3.5	277	9	AA491505	AA491505 ab23e04.r
576	46	3.5	245	9	AA274319	AA274319 TGESTz225	650	46	3.5	277	11	BC033874	BC033874 Homo sapi
577	46	3.5	245	12	BI674221	BI674221 saf16f03.	651	46	3.5	278	13	BU536318	BU536318 AGENCOURT
578	46	3.5	245	12	BI783989	BI783989 kh28c09.y	652	46	3.5	278	14	CD514668	CD514668 AGENCOURT
579	46	3.5	245	12	BJ392311	BJ392311 BJ392311	C 653	46	3.5	279	9	AU261874	AU261874 AU261874
580	46	3.5	245	13	BY964867	BY964867 sat03f06.	654	46	3.5	279	9	AI442860	AI442860 ea267g12.x
581	46	3.5	247	9	AW327958	AW327958 dr03b09.x	655	46	3.5	279	9	AU261874	AU261874 AU261874
582	46	3.5	247	10	BG381878	BG381878 296803.MA	656	46	3.5	280	12	BM967558	BM967558 ph47e09.y
583	46	3.5	247	10	BE015532	BE015532 EST758.MA	657	46	3.5	280	14	CA692707	CA692707 wlm96.pk0
584	46	3.5	247	13	BQ701706	BQ701706 NXST 118	C 657	46	3.5	281	9	AI445712	AI445712 tj09a03.x
585	46	3.5	247	13	BU555250	BU555250 AGENCOURT	658	46	3.5	281	9	AW307035	AW307035 sf52a02.y
586	46	3.5	248	14	CA454609	CA454609 AGENCOURT	659	46	3.5	282	9	AU085913	AU085913 AU085913
587	46	3.5	249	12	BM055889	BM055889 l84c02.y	660	46	3.5	282	9	AW346974	AW346974 29918.MAR
588	46	3.5	249	14	CB059948	CB059948 4010309.B	661	46	3.5	282	9	AA596374	AA596374 vo38a11.r

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Mon Nov 10 09:22:00 2003

C 662	46	3.5	282	10	BE717689	BE717689 RC4-HT078	735	46	3.5	312	9	AW315272	AW315272 12447 MAR
663	46	3.5	283	9	AW569888	AW569888 si82h01.Y	736	46	3.5	314	9	AW711133	AW711133 vt56c09.X
664	46	3.5	284	9	AW153282	AW153282 se43g05.Y	737	46	3.5	314	9	BQ963970	BQ963970 AGENCOURT
665	46	3.5	284	12	BI759197	BI759197 603042623	738	46	3.5	314	13	BQ902882	BQ902882 AGENCOURT
666	46	3.5	285	9	AA253875	AA253875 sw75g08.X	739	46	3.5	315	12	BI677287	BI677287 i888d02.Y
667	46	3.5	285	9	AW733216	AW733216 kv71e02.Y	740	46	3.5	315	14	CB221907	CB221907 i1u21e10
C 668	46	3.5	285	12	BG991092	BG991092 MR2-HT118	741	46	3.5	316	14	CA935172	CA935172 sau49g02.
C 669	46	3.5	286	9	AI463395	AI463395 uc39g01.X	742	46	3.5	317	9	AW734601	AW734601 vq56h08.X
670	46	3.5	286	10	BE059871	BE059871 sn38c03.Y	743	46	3.5	317	9	AW020076	AW020076 df03g12.Y
671	46	3.5	286	10	BE68240	BE68240 156839 MA	744	46	3.5	317	10	BG884572	BG884572 186111 MA
672	46	3.5	287	12	BM940924	BM940924 UI-M-BZ1-	745	46	3.5	318	9	AW289167	AW289167 xfl14d06.X
673	46	3.5	287	12	CB021432	CB021432 PX71b05.Y	746	46	3.5	319	9	BG895791	BG895791 359422 MA
674	46	3.5	287	14	CB021432	CB021432 PX71b05.Y	747	46	3.5	319	12	BG895791	BG895791 359422 MA
675	46	3.5	288	13	BM263626	BM263626 BW263626	748	46	3.5	320	13	BQ197279	BQ197279 NXU1v11.H
676	46	3.5	288	10	BE563292	BE563292 BW563292	749	46	3.5	320	9	AI799244	AI799244 tw55c06.X
677	46	3.5	289	12	BI119510	BI119510 AR18A4 Po	750	46	3.5	321	10	BG452334	BG452334 NF086D08L
C 678	46	3.5	290	13	BU760965	BU760965 sas61a07.	751	46	3.5	321	12	BM434047	BM434047 1RT01E01
679	46	3.5	290	14	CA819681	CA819681 sau74d06.	752	46	3.5	321	14	CB047814	CB047814 NISC GJ01
680	46	3.5	291	9	AA217076	AA217076 mu91a08.X	753	46	3.5	322	9	AI397120	AI397120 fh16g12.X
681	46	3.5	291	9	AW097129	AW097129 AU097129	754	46	3.5	322	9	AW089379	AW089379 xk04g04.X
682	46	3.5	291	10	BE667534	BE667534 151936 MA	755	46	3.5	322	13	BG851632	BG851632 AGENCOURT
683	46	3.5	292	13	BQ963260	BQ963260 AGENCOURT	756	46	3.5	323	9	AV996007	AV996007 AV996007
684	46	3.5	292	13	AL135517	AL135517 DKEPZP762K	757	46	3.5	323	13	BQ629310	BQ629310 sap87d07.
685	46	3.5	293	13	BU775395	BU775395 SUEBLG12	758	46	3.5	323	14	CA754771	CA754771 BR0300060
686	46	3.5	293	14	R44339	R44339 YG35g12.s1	759	46	3.5	323	14	CA754771	CA754771 NISC GJ01
C 687	46	3.5	294	9	AW079148	AW079148 xa96d06.X	760	46	3.5	324	9	AA267381	AA267381 m294c06.X
688	46	3.5	294	14	CB522658	CB522658 UI-M-GK0-	761	46	3.5	324	10	BW813364	BW813364 sk68h10.Y
689	46	3.5	295	14	CA314283	CA314283 UI-CF-FNO	762	46	3.5	324	10	BW813364	BW813364 sk68h10.Y
690	46	3.5	295	14	CB344591	CB344591 CA48EN000	763	46	3.5	324	10	BW813364	BW813364 sk68h10.Y
691	46	3.5	296	10	BG155473	BG155473 sbd4e12.	764	46	3.5	325	9	AI682759	AI682759 w565n05.X
692	46	3.5	296	10	BE059560	BE059560 sn33g02.Y	765	46	3.5	325	9	AI682759	AI682759 w565n05.X
693	46	3.5	296	12	BI101686	BI101686 602887513	766	46	3.5	325	9	AW095408	AW095408 AU095408
694	46	3.5	297	14	CB102254	CB102254 MWV SQ006	767	46	3.5	325	9	AW101005	AW101005 sq64d10.Y
C 695	46	3.5	298	14	CB102254	CB102254 MWV SQ006	768	46	3.5	325	9	AA428025	AA428025 zw32h04.X
C 696	46	3.5	299	12	BI023212	BI023212 CMO-WT039	769	46	3.5	325	12	BM966203	BM966203 k003f04.Y
C 697	46	3.5	299	12	BI945688	BI945688 sc51h07.Y	770	46	3.5	325	12	BM966203	BM966203 k003f04.Y
698	46	3.5	299	13	BUS36259	BUS36259 AGENCOURT	771	46	3.5	325	13	BQ215227	BQ215227 AGENCOURT
699	46	3.5	299	14	CA465028	CA465028 AGENCOURT	772	46	3.5	325	14	CD570807	CD570807 kb77a02.Y
700	46	3.5	299	14	CB701277	CB701277 AGENCOURT	773	46	3.5	326	9	AA271595	AA271595 vt74f02.X
701	46	3.5	300	9	AL367874	AL367874 MCB19G12	774	46	3.5	326	12	BM566378	BM566378 vt74f02.X
C 702	46	3.5	300	13	BQ96800	BQ96800 NISC R922	775	46	3.5	327	12	BI381584	BI381584 BFLG1 003
C 703	46	3.5	301	12	BI744744	BI744744 rk91h05.Y	776	46	3.5	327	12	BI381584	BI381584 BFLG1 003
704	46	3.5	301	12	BM022994	BM022994 ide64h01.Y	777	46	3.5	327	12	BI381584	BI381584 BFLG1 003
705	46	3.5	302	9	AA830022	AA830022 sc43h08.s	778	46	3.5	328	13	BU770654	BU770654 SUECVB02
C 706	46	3.5	302	9	AA830022	AA830022 sc43h08.s	779	46	3.5	328	13	BU770654	BU770654 SUECVB02
C 707	46	3.5	302	10	BG156543	BG156543 sab10h11.	780	46	3.5	329	13	BQ126177	BQ126177 i114c03.Y
708	46	3.5	302	12	BM85442	BM85442 sam01a07.	781	46	3.5	329	13	BQ126177	BQ126177 i114c03.Y
709	46	3.5	303	14	C93132	C93132 C93132 Dict	782	46	3.5	329	14	CD251734	CD251734 sau59g07.
710	46	3.5	303	14	W54462	W54462 md06a11.r1	783	46	3.5	330	9	AL039771	AL039771 DKEPZP34P
711	46	3.5	304	13	BUS84131	BUS84131 1849527F6	784	46	3.5	330	9	AA212898	AA212898 mw82a10.X
712	46	3.5	304	14	CA336817	CA336817 NISC 1v05	785	46	3.5	330	10	BG121999	BG121999 602351658
713	46	3.5	305	10	AW959910	AW959910 EST371981	786	46	3.5	330	13	BU772321	BU772321 SUEBOG04
714	46	3.5	305	12	BI037699	BI037699 949017C09	787	46	3.5	331	12	BI886911	BI886911 ZF637-1-0
715	46	3.5	305	14	CA803302	CA803302 ESG01C.E	788	46	3.5	331	13	BU776295	BU776295 SUEGLD05
716	46	3.5	306	9	AL130841	AL130841 x011f03.s	789	46	3.5	332	12	BM690141	BM690141 UI-E-CL0-
C 717	46	3.5	306	14	C90836	C90836 C90836 Dict	790	46	3.5	332	12	BI345602	BI345602 374477 MA
C 718	46	3.5	307	14	CD052334	CD052334 EST1593 Z	791	46	3.5	333	12	BI972373	BI972373 sag90e12.
C 719	46	3.5	307	14	CD052334	CD052334 EST1593 Z	792	46	3.5	333	12	BI972373	BI972373 sag90e12.
720	46	3.5	307	13	BU767512	BU767512 x101d10.X	793	46	3.5	334	9	AW095405	AW095405 AU095405
721	46	3.5	308	9	AW277341	AW277341 up11a05.Y	794	46	3.5	334	12	BI426914	BI426914 sag09a04.
722	46	3.5	309	13	BM761114	BM761114 sas63c06.	795	46	3.5	334	12	BI426914	BI426914 sag09a04.
723	46	3.5	309	14	CA819720	CA819720 sau74h11.	796	46	3.5	335	13	BQ668830	BQ668830 g11e1d2.
724	46	3.5	310	2	HSN083149	HSN083149 Homo sapi	797	46	3.5	335	13	BQ668830	BQ668830 g11e1d2.
725	46	3.5	310	12	BI535118	BI535118 398454 MA	798	46	3.5	337	9	AL714923	AL714923 AL714923
726	46	3.5	310	12	BI535118	BI535118 398454 MA	799	46	3.5	337	9	AL714923	AL714923 AL714923
727	46	3.5	310	12	BI535118	BI535118 398454 MA	800	46	3.5	337	13	BUS689756	BUS689756 AGENCOURT
728	46	3.5	310	12	BI535118	BI535118 398454 MA	801	46	3.5	338	9	AW100848	AW100848 s062b10.Y
729	46	3.5	310	13	BU946050	BU946050 AGENCOURT	802	46	3.5	338	9	AW100848	AW100848 s062b10.Y
730	46	3.5	310	14	CB697053	CB697053 AGMNNUC:U	803	46	3.5	339	13	BU761175	BU761175 sas54b08.
C 731	46	3.5	311	14	CB933326	CB933326 x128e04.Y	804	46	3.5	339	10	BF536278	BF536278 602051927
732	46	3.5	311	14	CB933326	CB933326 x128e04.Y	805	46	3.5	339	10	BF536278	BF536278 602051927
733	46	3.5	311	14	CB933326	CB933326 x128e04.Y	806	46	3.5	339	13	BU677294	BU677294 UI-CF-DU1
C 734	46	3.5	312	9	AW197005	AW197005 xb14c07.X	807	46	3.5	340	9	AT765089	AT765089 w148a09.X

808	46	3.5	340	12	BM569511	BM569511 kj62f10.Y	881	46	3.5	367	9	AL643167	AL643167
C 809	46	3.5	340	13	B0799704	B0799704 EST 1873	882	46	3.5	367	14	CB000271	CB000271 S345T.G06
810	46	3.5	340	13	B0799704	B0799704 EST 1873	882	46	3.5	367	14	CB000271	CB000271 S345T.G06
811	46	3.5	340	14	B0799704	B0799704 EST 1873	883	46	3.5	368	13	BY673667	BY673667 BY673667
812	46	3.5	340	14	CD351386	CD351386 UI-M-G10-	884	46	3.5	368	14	CD392542	CD392542 Gm ck1173
813	46	3.5	341	13	B0762496	B0762496 sap28b05.	885	46	3.5	369	9	AA423575	AA423575 ve7g05.r
814	46	3.5	341	14	CB079723	CB079723 hp75f04.b	886	46	3.5	369	10	BE235634	BE235634 143193.MA
815	46	3.5	342	14	CA802780	CA802780 sau42a09.	887	46	3.5	369	12	BM569755	BM569755 1n97b02.Y
C 816	46	3.5	342	9	A1362522	A1362522 qv72d07.x	888	46	3.5	370	10	BE684533	BE684533 186001.MA
817	46	3.5	343	10	B043626	B043626 sv39b03.Y	889	46	3.5	371	9	AV760402	AV760402 AV760402
818	46	3.5	343	14	CA337467	CA337467 NISC_lw01	C 890	46	3.5	371	9	AW335588	AW335588 S49B4.AGS
819	46	3.5	343	14	CA337467	CA337467 NISC_lw01	891	46	3.5	371	9	AA390241	AA390241 CP8ST.231
820	46	3.5	344	14	CB693218	CB693218 ELQ1N0310	892	46	3.5	371	10	BG632517	BG632517 G099846.5
821	46	3.5	344	9	AA033195	AA033195 mi39h01.r	893	46	3.5	371	14	CB075829	CB075829 h251h02.b
C 822	46	3.5	344	9	AA611786	AA611786 v085h06.r	C 894	46	3.5	372	9	AA804302	AA804302 nw31h11.s
823	46	3.5	344	14	CB084212	CB084212 hq1f11.b	895	46	3.5	372	10	BG382618	BG382618 298583.MA
824	46	3.5	345	9	AA616335	AA616335 v65a10.r	896	46	3.5	373	12	B1376731	B1376731 BFLG3.000
C 825	46	3.5	345	14	CB705871	CB705871 AMGNNUC:U	C 897	46	3.5	373	10	BM495109	BM495109 JPCGB1.4
826	46	3.5	346	12	BJ207280	BJ207280 BJ207280	898	46	3.5	373	14	CA486557	CA486557 WE4333.B
827	46	3.5	347	14	CB523220	CB523220 UI-M-GK0-	899	46	3.5	373	14	CA819740	CA819740 sau75d01.
828	46	3.5	348	9	AA038807	AA038807 mi95b04.r	C 900	46	3.5	374	9	AV712612	AV712612 AV712612
829	46	3.5	348	9	AL644569	AL644569 AL644569	C 901	46	3.5	374	9	CA668301	CA668301 w1su1.pk0
830	46	3.5	348	10	BG383179	BG383179 301132.MA	902	46	3.5	374	14	CB094952	CB094952 h277c02.b
831	46	3.5	349	12	B1378856	B1378856 BFLG1.000	903	46	3.5	375	12	BI704162	BI704162 x063g04.Y
832	46	3.5	349	14	CA302118	CA302118 taal0601.	904	46	3.5	375	14	CB830500	CB830500 r117h03.Y
833	46	3.5	349	14	CA764732	CA764732 AP53.Pdf	905	46	3.5	377	10	BG389157	BG389157 602444977
834	46	3.5	350	12	BM905276	BM905276 AGENCOURT	906	46	3.5	377	12	BM525528	BM525528 sal29a11.
C 835	46	3.5	350	13	BQ398164	BQ398164 NISC.mo05	C 907	46	3.5	377	13	BY669070	BY669070 BY669070
836	46	3.5	351	14	CB781081	CB781081 AMGNNUC:S	C 908	46	3.5	379	9	AI291103	AI291103 qml0d01.x
837	46	3.5	351	9	AW485985	AW485985 69165.MAR	C 909	46	3.5	379	9	AL047570	AL047570 DKP2586E
838	46	3.5	352	9	AI292655	AI292655 GH15605.5	C 910	46	3.5	379	13	BQ394195	BQ394195 NISC.rg07
839	46	3.5	352	13	BY392467	BY392467 BY392467	911	46	3.5	379	14	C99698	C99698 C99698.Rice
C 840	46	3.5	353	9	AA218987	AA218987 zrl1905.s	912	46	3.5	380	9	AO076356	AO076356 AU076356
841	46	3.5	353	9	AW192300	AW192300 xl84a11.x	913	46	3.5	380	12	BG894653	BG894653 355348.MA
842	46	3.5	354	9	AW192300	AW192300 xl84a11.x	914	46	3.5	381	14	BY669201	BY669201 BY669201
843	46	3.5	354	12	BM886657	BM886657 sam19e02.	915	46	3.5	381	14	C99068	C99068 C99068.Rice
844	46	3.5	354	13	BQ453941	BQ453941 sap02e03.	916	46	3.5	381	14	CB809622	CB809622 AMGNNUC:S
845	46	3.5	354	13	BQ623840	BQ623840 USDA.PP.0	917	46	3.5	382	12	BM892208	BM892208 R507b10.Y
846	46	3.5	355	9	AW632430	AW632430 sm10c09.Y	918	46	3.5	383	13	BY465286	BY465286 BY465286
C 847	46	3.5	355	13	BQ078177	BQ078177 fY85d08.Y	919	46	3.5	384	10	BEG29296	BEG29296 uu36c07.Y
C 848	46	3.5	355	13	BQ393254	BQ393254 NISC.rg02	920	46	3.5	384	12	BI377250	BI377250 BFLG3.001
849	46	3.5	355	13	BQ634559	BQ634559 NRRV070.D	921	46	3.5	384	12	CB094493	CB094493 h270f09.b
C 850	46	3.5	355	14	CD415635	CD415635 Gm ck5345	922	46	3.5	384	14	CD414752	CD414752 Gm ck4753
C 851	46	3.5	356	9	AI976772	AI976772 EST271366	C 923	46	3.5	385	9	AV975649	AV975649 AV975649
C 852	46	3.5	356	9	AW569308	AW569308 sl76d07.Y	924	46	3.5	385	12	BM889208	BM889208 R507b10.Y
C 853	46	3.5	357	14	CB285667	CB285667 CMD22.A08	925	46	3.5	385	12	BY377795	BY377795 BFLG3.001
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857	46	3.5	358	14	CB018582	CB018582 P49C02.Y	C 929	46	3.5	387	9	AI457343	AI457343 t173b03.X
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859	46	3.5	359	13	BQ155641	BQ155641 NF08F011	931	46	3.5	388	12	BM155487	BM155487 fw06c08.Y
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C 862	46	3.5	360	9	AI440261	AI440261 tJ01d06.x	934	46	3.5	390	9	AW635129	AW635129 b129f12.w
863	46	3.5	360	9	AW133495	AW133495 sel19g12.Y	935	46	3.5	390	14	C90886	C90886 C90886.Dict
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865	46	3.5	361	9	AU174992	AU174992 AU174992	937	46	3.5	391	13	BUS08635	BUS08635 AGENCOURT
866	46	3.5	361	9	AV763278	AV763278 AV763278	938	46	3.5	391	13	BUS41473	BUS41473 AGENCOURT
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869	46	3.5	362	12	BM346610	BM346610 kx65d12.Y	941	46	3.5	392	12	BI379142	BI379142 BFLG1.000
870	46	3.5	362	13	BW254378	BW254378 BW254378	942	46	3.5	392	13	BY392281	BY392281 BY392281
871	46	3.5	363	9	AA230383	AA230383 mv73a12.r	943	46	3.5	392	14	CB019118	CB019118 PX73e09.Y
C 872	46	3.5	363	9	AA858206	AA858206 ce43c09.s	944	46	3.5	392	14	CB019118	CB019118 PX73e09.Y
873	46	3.5	364	9	AW681618	AW681618 AW681618	945	46	3.5	392	14	CB409731	CB409731 NISC.nc06
874	46	3.5	364	14	CA348393	CA348393 679694.NC	C 946	46	3.5	393	9	AI913351	AI913351 wallb12.x
875	46	3.5	364	14	CA819802	CA819802 sau76c10.	947	46	3.5	393	10	BG112028	BG112028 602281873
876	46	3.5	364	14	CB074971	CB074971 nx13c05.b	C 948	46	3.5	393	10	BG631848	BG631848 cc-esf1GL
877	46	3.5	365	9	AI158230	AI158230 ud21g12.r	949	46	3.5	393	10	BE877326	BE877326 601485559
878	46	3.5	365	9	AI854961	AI854961 605094G02	950	46	3.5	393	14	CB217890	CB217890 NISC.pb05
879	46	3.5	365	12	BM285328	BM285328 pb12e03.Y	951	46	3.5	394	14	CD487433	CD487433 Gm cF1136
880	46	3.5	366	10	BE419061	BE419061 WWR018.E6	952	46	3.5	395	10	BFL81585	BFL81585 WR2-C1012
							953	46	3.5	395	12	BI381051	BI381051 BFLG1_002

954	3.5	396	9	AU263111	AU263111	JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
955	3.5	397	9	AW058913	fes0e09.x	COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maize.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pac Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
956	3.5	397	10	AW989051	uq12e08.Y	FEATURES	Location/Qualifiers
957	3.5	397	10	BE752330	204689.MA	source	1. .1342
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959	3.5	397	13	BQ628137	sac01f12	/mol_type="mRNA"	
960	3.5	397	13	BQ691974	AGENCOURT	/db_xref="MaizeDB:634127"	
961	3.5	398	9	A1635082	tz23b04.x	/db_xref="taxon:4577"	
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963	3.5	398	13	BU774392	SJRGKE04	/notes="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"	
964	3.5	399	9	A1118304	ue39h02.x	BASE COUNT	361 a 315 c 343 g 323 t
965	3.5	399	9	AA396149	AA396149	ORIGIN	
966	3.5	399	10	AA396149	AA396149	Query Match	100.0%; Score 1326; DB 11; Length 1342;
967	3.5	399	10	AA396149	AA396149	Best Local Similarity	100.0%; Pred. No. 7,8e-175;
968	3.5	399	14	CB700255	ANGNOC:N	Matches 1326; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
969	3.5	400	9	AU060236	sh32b03.Y		
970	3.5	400	9	AW596423	sj12c04.Y		
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973	3.5	400	14	CB089323	qs07g07.b		
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975	3.5	402	9	AU095196	AU095196		
976	3.5	402	10	BF793137	602254140		
977	3.5	402	14	CA803718	ESG0110b.		
978	3.5	403	9	AA831733	oc93a04.s		
979	3.5	403	13	EQ801653	WHE2817.A		
980	3.5	404	9	AW066606	683003H03		
981	3.5	404	12	BI494234	BI494234		
982	3.5	404	12	BI902057	id17b12.Y		
983	3.5	404	12	BM922557	AGENCOURT		
984	3.5	404	13	BY392337	BY392337		
985	3.5	404	9	AU033042	AU033042		
986	3.5	405	14	CA813308	sau72807.		
987	3.5	406	13	BU188267	AGENCOURT		
988	3.5	406	13	BU593872	AGENCOURT		
989	3.5	406	13	BU925902	BU925902		
990	3.5	407	9	AA810605	ob64c09.s		
991	3.5	407	9	AL718978	AL718978		
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ALIGNMENTS

RESULT 1	AY106146	1342 bp	linear	HTC 16-OCT-2002
LOCUS	AY106146			
DEFINITION	Zea mays PC0074795 mRNA sequence.			
ACCESSION	AY106146			
VERSION	AY106146.1	GI:21209224		
KEYWORDS	HTC.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogoneae; Zea.			
AUTHORS	1 (bases 1 to 1342)			
TITLE	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.			
JOURNAL	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes			
REFERENCE	Unpublished (2002)			
AUTHORS	2 (bases 1 to 1342)			
TITLE	Coe, E.H.			
	Direct Submission			

QY	661	TTGATGAGGATGAAGAAATCTCAGTGGCAAGCGTAATTGATCTGAATCTTACTGGCGTC	720
Db	677	TTGATGAGGATGAAGAAATCTCAGTGGCAGACGTAATTGATCTGAATCTTACTGGCGTC	736
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QY	781	AACATTGCATCTGTAGTTGGTCTTACTGCGAATGTTGGCCAAAGCTAATAATATAGCGCAGCC	840
Db	797	AACATTGCATCTGTAGTTGGTCTTACTGCGAATGTTGGCCAAAGCTAATAATATAGCGCAGCC	856
QY	841	AAGCTGGAGTGATTGGTTTCCAAAAACAGTTCGCCGGAGTATGCAAGCAGAAATATC	900
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QY	1141	CTTTTGTGTCGACATTAATGTTGAACACCCCTTGTGTGTCACGGCGGATTTTGGACAACAA	1200
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QY	1261	AGTTGGAATCTGGGTTTTCTGTGTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1320
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Db	1337	AAAAAA 1342	

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LOCUS       CB604782                linear   EST 16-MAY-2003
DEFINITION  3529_1_61_1_C02.y 1 3529 - 2 mm ear tissue from Schmidt and Hake
            labs Zea mays cDNA, mRNA sequence.
ACCESSION   CB604782
VERSION     CB604782.1    GI:29544402
KEYWORDS    EST.
SOURCE      Zea mays
ORGANISM    Zea mays
REFERENCE   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
AUTHORS     1 (bases 1 to 646)
TITLE       Walbot,V.
COMMENT     Maize ESTs from various cDNA libraries sequenced at Stanford
            University
            Unpublished
            Contact: walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2327

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FEATURES
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BASE COUNT
ORIGIN

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Query Match	46.8%;	Score 620;	DB 14;	Length 646;				
Best Local Similarity	100.0%;	Pred. No. 2.5e-77;						
Matches 620;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
Qy	51	GCTCTGCTCGTCA	CGGCTCAAA	TACTCGGCTGCA	ATCTCCAAAGCACACTGCTCCTCT	110		
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Qy	231	CGCGGCTTC	CGCGGGGTT	TGCTCA	GGTTGGTGA	GCGCGCGCTTCTCTCCAC	290	
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Qy	291	GCTGCGGTC	CGGCGGTCT	CTCGGTG	CAACCCATG	TGCTGTGTAACAAGC	350	
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Qy	351	AGTTGTA	AAAAGATGCT	TACCAAGCT	CGAAGCTC	CAAGTTGTTGTTTACAGGTGCATCTAG	410	
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Qy	411	AGGGATTG	TAGGCAACT	GTCTTAG	CCCTTG	GAAGAAGCAGGATGCAAGGTTCTGTTAAA	470	
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Qy	471	CTATGCCCGGT	CTCTGAAAGAGCT	CAAGAGCT	CTC	CAAGAGATGTAAGCATCTGGTG	530	
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Db	507	TGAGGCTAT	CACCTTCG	GAGGAGATGTTT	CAAAAGAGCT	GTAGTGTATGATGA	566	
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LOCUS
BQ293972 600 bp mRNA linear EST 15-MAY-2002
DEFINITION
1091024E01.v3 1091 - Immature ear with common ESTs screened by

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Schmidt lab Zea mays cDNA, mRNA sequence.
BQ293972.1 GI:20802922
EST.
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1091024 row: E column: 01.
Location/Qualifiers
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/clone_lib="1091 - Immature ear with common ESTs screened
by Schmidt lab"
/notes="Organ: Immature ear; Vector: pAD-GAL4; Site 1:
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Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 778 ATCAACATTGCATCTGTAGTTGGTCTTACTGGCAATGTTGCCAAGCTAATTATAGCGCA 837
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DB 142 GCCAAGCTGAGTGATGTTTCACAAAAACAGTTCACAGGGAGTATGCAAGCAGAAAT 201
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DB 202 ATCAATGTGATGCTATTGACACAGGTTTCATTCATCTGATATGACGCGCACTTGA 261
QY 958 GAAGAGCTTGAGAGAGAAATCTTGTCAACCAATTCGTTAGGAGATATGCGCAACAGAG 1017
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QY 1078 CAGTGTCTTCAATGACGGGGGATGTAATGTAAGATTGAGTTGACTTGTGACTCTT 1137
DB 382 CAGTGTCTTCAATGACGGGGGATGTAATGTAAGATTGAGTTGACTTGTGACTCTT 441
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442 CTACTTTTGTGAGCAATTAATGTTGAACACCCCTTGTGTGACGGCGGATTTTGACAA 501
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1258 GGAAGTTGAAA 1268
562 GGAAGTTGAAA 572
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BU092521
LOCUS
DEFINITION
946152D04.y1 946 - tassell primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION
BU092521
VERSION
BU092521.1 GI:22542083
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 557)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946152 row: D column: 04.
Location/Qualifiers
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inflorescence development"
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lab"
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Site 2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 Kb with a 1 Kb average."
BASE COUNT 168 a 96 c 137 g 156 t
ORIGIN
Query Match 41.5%; Score 550; DB 13; Length 557;
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Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TCTTCCTTTGTACACAGGCTGCACAAAGTAATGTAAGAAAGAGAAAGGGAATAATTA 60
QY 779 TCAACATTGCATCTGAGTTGGTCTTACTGGCAATGTTGCCAAGCTAATTATAGCGCAG 838
DB 61 TCAACATTGCATCTGAGTTGGTCTTACTGGCAATGTTGCCAAGCTAATTATAGCGCAG 120
QY 839 CCAAGGCTGGAGTGATGTTGTTTCAAAAAACAGTTCGCCAGGGAGTATCAAGCAGAAATA 898
DB 121 CCAAGGCTGGAGTGATGTTGTTTCAAAAAACAGTTCGCCAGGGAGTATCAAGCAGAAATA 180

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Plate: 946117 ROW: H Column: 09.

FEATURES

Source:

Location/Qualifiers
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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to inflorescence development"
/lab_host="XL0LR"
/clone_lib="946 - tassal primordium prepared by Schmidt lab"
/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
180 a 108 c 159 g 170 t 1 others

Query Match 36.8%; Score 488; DB 13; Length 618;
Best Local Similarity 100.0%; Pred. No. 3.9e-59;
Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 718 GTCTTCTTTGTACACAGGCTGCAACAAAAGTAATCATGAAAAGAGAAAGGAGAAAAT 777
Db |
74 GTCTTCTTTGTACACAGGCTGCAACAAAAGTAATCATGAAAAGAGAAAGGAGAAAAT 133
QY 778 ATCAACATTGCATCTGTAGTGTCTTACTGGCAATGTTGGCAAGCTAATTATAGCGCA 837
Db |
134 ATCAACATTGCATCTGTAGTGTCTTACTGGCAATGTTGGCAAGCTAATTATAGCGCA 193
QY 838 GCCAAGCGTGGAGTATGTTTTCACAAAACAGTTGCCAGGAGTATCGACGAGAAAT 897
Db |
194 GCCAAGCGTGGAGTATGTTTTCACAAAACAGTTGCCAGGAGTATCGACGAGAAAT 253
QY 898 ATCAATGTGAATGCTATTGCACAGGTTTCATTGCTATGATGATGCTCCGAACTTGA 957
Db |
254 ATCAATGTGAATGCTATTGCACAGGTTTCATTGCTATGATGATGCTCCGAACTTGA 313
QY 958 GAAGAGCTTGAGAGAAAATCTTGTCAACCAATTCGTTAGGAGATATGCCAACACAGAG 1017
Db |
314 GAAGAGCTTGAGAGAAAATCTTGTCAACCAATTCGTTAGGAGATATGCCAACACAGAG 373
QY 1018 GAAGTTGACAGGTTGTCAGTCTCTGCGCCCTTAACCCCGCAGCTAGCTATATAGCTGA 1077
Db |
374 GAAGTTGACAGGTTGTCAGTCTCTGCGCCCTTAACCCCGCAGCTAGCTATATAGCTGA 433
QY 1078 CAGGTGCTTTACAAATTGACGGAGGATGTAATGTAAGATTTCAGTTAGCTTGCATGCACTT 1137
Db |
434 CAGGTGCTTTACAAATTGACGGAGGATGTAATGTAAGATTTCAGTTAGCTTGCATGCACTT 493
QY 1138 CTACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTGACGGCGGATTTTGACAAA 1197
Db |
494 CTACTTTTGTCTGAGCATTTAATGTTGAACACCCCTTGTGTGACGGCGGATTTTGACAAA 553
QY 1198 CAAATTAG 1205
Db |
554 CAAATTAG 561

RESULT 7
CD484893/c

LOCUS CD484893 659 bp mRNA linear EST 04-JUN-2003
DEFINITION 3529_1_110_1_c12.x.1 3529 - 2 mm ear tissue from Schmidt and Hake

ACCESSION CD484893

VERSION CD484893.1

KEYWORDS EST. GI:31406161

SOURCE Zea mays

ORGANISM Zea mays

DEFINITION Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS

TITLE

JOURNAL

COMMENT

COMMENTS

COMMENTS

COMMENTS

COMMENTS

COMMENTS

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QY	640	GGGATTACACGACACACATTTGTTGATGAGATGAGAAATCTCAGTGGCAACACCTAATT	639
Db	440	GGGATTACACGACACACATTTGTTGATGAGATGAGAAATCTCAGTGGCAACACCTAATT	499
QY	700	GATCTGAATCTTACTGGCGTCTTCCCTTTGTACACAGGCTGCAACAAATGATGATGAAA	759
Db	500	GATCTGAATCTTACTGGTCTTCTCTTTGTACACAGGCTGCAACAAATGATGATGAAA	559
QY	760	AACGAAAGGGGAAAATTAATCAACATTCATCTGTAGTTGGTCTTACTGGCAATGTTGGC	819
Db	560	AACGAAAGGGGAAAATTAATCAACATTCATCTGTAGTTGGTCTTACTGGCAATGTTGGC	619
QY	820	CAAGCTTAATTAATAGCGCAGC	839
Db	620	CAAGCTTAATTAATAGCGCAGC	639
RESULT 9			
CD510389		457 bp	linear
LOCUS		3529_1_110_1_C12.y_1	3529 - 2 mm ear tissue from Schmidt and Hake
DEFINITION		Zeas Zea mays cDNA, mRNA sequence.	
ACCESSION		CD510389	
VERSION		CD510389.1	GI:31440958
KEYWORDS		EST.	
SOURCE		Zeas mays	
ORGANISM		Zeas mays	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.	
AUTHORS		Walbot,V.	
TITLE		Maize ESTs from various cDNA libraries sequenced at Stanford University	
JOURNAL		Unpublished	
COMMENT		Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 3529_1_110_1 row: C column: 12.	
FEATURES		Location/Qualifiers	
source		1..457	
		/organism="Zea mays"	
		/mol_type="mRNA"	
		/cultivar="B73"	
		/db_xref="taxon:4577"	
		/tissue_type="ear"	
		/dev_stage="2 mm"	
		/lab_host="E. coli XL0LR"	
		/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake labs"	
		/note="Organ: ear; Vector: PAD-GAL4-2.1; Site: 1: EcoRI; Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu amplified. Ampicillin is the selection marker."	
BASE COUNT		73 a 164 c 122 g 98 t	
ORIGIN			
Query Match		34.5%; Score 457; DB 14; Length 457;	
Best Local Similarity		100.0%; Pred. No. 9.6e-35;	
Matches		457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	23	GTCCCCCAATAGACTCTCCCATCCGTCGTCTGTCGTCACGGCTCAAAATCTCCGCC	82
Db	1	GTCCCCCAATAGACTCTCTCCCATCCGTCGTCTGTCGTCACGGCTCAAAATCTCCGCC	60
QY	83	TGCATCTCAAAGCACACTGCTCCCTCTGGCTTCCGCTCCTCTTGGGTCCTTCGCT	142
Db	61	TGCATCTCAAAGCACACTGCTCCCTCTGGCTTCCGCTCCTCTTGGGTCCTTCGCT	120

143 CCCGACGCCCTCATGTCACCGCCGCGCCACCGCAGCAGCAGCAGCTCTCTCCC 202
 121 CCCGACGCCCTCATGTCACCGCCGCGCCACCGCAGCAGCAGCAGCTCTCTCCC 180
 203 CGGTCGCGGTGGAGCAGCGCGGGCGCGCGCGCTCCCGCGGGGTTCTGTCAGTTTG 262
 181 CGGTCGCGGTGGAGCAGCGCGGGCGCGCGCGCTCCCGCGGGGTTCTGTCAGTTTG 240
 263 GTGAGGCGCGCGCGCTCTCTCTCCACGCTGCGGTCCGCGCGGGTTCCTGCTGTC 322
 241 GTGAGGCGCGCGCGCTCTCTCTCCACGCTGCGGTCCGCGCGGGTTCCTGCTGTC 300
 323 AAACCCATGTTGCTGCTCTGCAACAGCAGTGTAAAGATGCTACCAAGCTGGAAGCTC 382
 301 AAACCCATGTTGCTGCTCTGCAACAGCAGTGTAAAGATGCTACCAAGCTGGAAGCTC 360
 383 CAGTGTGTTGTTACAGTGTCATCTAGAGGATGTTAGGCAACTGCTCTAGCCCTTG 442
 361 CAGTGTGTTGTTACAGTGTCATCTAGAGGATGTTAGGCAACTGCTCTAGCCCTTG 420
 443 GAAAGCAGGATGCAAGTTCCTGTAACACTATGCCCCG 479
 421 GAAAGCAGGATGCAAGTTCCTGTAACACTATGCCCCG 457

RESULT 10
 BU092794 539 bp mRNA linear EST 29-AUG-2002
 LOCUS 946157G10.y1 946 - tassell primordium prepared by Schmidt lab Zea
 DEFINITION mays cDNA, mRNA sequence.

ACCESSION BU092794
 VERSION BU092794.1 GI:22542341
 KEYWORDS EST.
 SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 539)

REFERENCE

AUTHORS Zea mays
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL University
 COMMENT Unpublished

Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221

Email: walbot@stanford.edu
 Plate: 946157 row: G column: 10.

FEATURES

source

Location/Qualifiers

1..539

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="OH43"

/db_xref="taxon:4577"

/tissue_type="tassels"

/dev_stage="just after the transition from vegetative to

inflorescence development"

/lab_host="XL0LR"

/clone_lib="946 - tassell primordium prepared by Schmidt

lab"

/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;

Site 2: XhoI; George Chuck dissected immature tassels

between 1mm and 3mm. Sharon Stanfield prepared the cDNA

library in HybriZAP. Sample insert size range was 350 bp

to 3 Kb with a 1 Kb average."

BASE COUNT 157 a 94 c 141 g 146 t 1 others

ORIGIN

Query Match 34.0%; Score 451; DB 13; Length 539;
 Best Local Similarity 99.8%; Pred. No. 5.5e-54;

Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 659 TGTGTAGAGATGAAGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATCTTACTGCG 718

Db 4 TGTGTAGAGATGAAGAAATCTCAGTGGCAAGACGTAATTTGATCTGAATCTTACTGCG 63

Qy 719 TCTTCCTTTGTACACAGCTGCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTA 778

Db 64 TCTTCCTTTGTACACAGCTGCAACAAAAGTAATGATGAAAAAGAGAAAGGAAAAATTA 123

Qy 779 TCACATGTCATCTGATGTTGGTCTTCTGCAATGTTGGCAAGCTTAATTTAGCCGAG 838

Db 124 TCACATGTCATCTGATGTTGGTCTTCTGCAATGTTGGCAAGCTTAATTTAGCCGAG 183

Qy 839 CCAGGCTGCAAGTGAATGTTTCAAAAAACAGTTGCCAGGAGTATGCAAGCAAGAATA 898

Db 184 CCAGGCTGCAAGTGAATGTTTCAAAAAACAGTTGCCAGGAGTATGCAAGCAAGAATA 243

Qy 899 TCAATGTGAATGCTATTGCAACAGGTTCAATGCAATGCAATGCAATGCAATGCAATG 958

Db 244 TCAATGTGAATGCTATTGCAACAGGTTCAATGCAATGCAATGCAATGCAATGCAATG 303

Qy 959 AAGAGCTTGAGAAAGAAATCTTGTCAACATTCGTTAGGAGATATGCGCCACCAAGG 1018

Db 304 AAGAGCTTGAGAAAGAAATCTTGTCAACATTCGTTAGGAGATATGCGCCACCAAGG 363

Qy 1019 AAGTTCAGGTTGGTGGAGTCTCTGCGCCCTTAACCCCGCAGCTAGCTATATGACTGGAC 1078

Db 364 AAGTTCAGGTTGGTGGAGTCTCTGCGCCCTTAACCCCGCAGCTAGCTATATGACTGGAC 423

Qy 1079 AGGTGCTTACAATGACGAGGATGTAATGTAAGATTGAGTTGAGTTGAGTTGAGTTG 1138

Db 424 AGGTGCTTACAATGACGAGGATGTAATGTAAGATTGAGTTGAGTTGAGTTGAGTTG 483

Qy 1139 TACTTTGCTGAGCAATTAATG 1160

Db 484 TACTTTGCTGAGCAATTAATG 505

RESULT 11

LOCUS

BO667989

946102B05.y1 946 - tassell primordium prepared by Schmidt lab Zea

mays cDNA, mRNA sequence.

ACCESSION BO667989

VERSION BO667989.1 GI:21809671

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 530)

REFERENCE 1

AUTHORS Walbot V

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL Unpublished

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 946102 row: E column: 05.

Location/Qualifiers

1..530

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="OH43"

/db_xref="taxon:4577"

/tissue_type="tassels"

/dev_stage="just after the transition from vegetative to

inflorescence development"
 /lab_host="XLOLR"
 /clone_lib="946 - tassal primordium prepared by Schmidt
 lab"
 /note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI;
 Site 2: XhoI; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybriZAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."
 BASE COUNT 154 a 95 c 132 g 147 t 2 others
 ORIGIN

Query Match 33.2%; Score 440; DB 13; Length 530;
 Best Local Similarity 100.0%; Pred. No. 1.8e-52;
 Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 721 TTCCTTTGTACACAGGCTGCAACAAAGTAATGATGAAAGAGAAAGGGAATAATTC 780
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 TTCCTTTGTACACAGGCTGCAACAAAGTAATGATGAAAGAGAAAGGGAATAATTC 60
 QY 781 AACATTGCACTGTAGTTGGTCTTACTGGCAATGTTGGCCAAAGCTAATTTATAGCGCAGCC 840
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 AACATTGCACTGTAGTTGGTCTTACTGGCAATGTTGGCCAAAGCTAATTTATAGCGCAGCC 120
 QY 841 AAGCGTGGAGTGATTGGTTTCACAAACACAGTTGCCAGGAGTATGCAAGCAGAAATATC 900
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 121 AAGCGTGGAGTGATTGGTTTCACAAACACAGTTGCCAGGAGTATGCAAGCAGAAATATC 180
 QY 901 ATGTGCAATGCTATTGCACAGGTTCAATGCACTGATATGACTGCCGAACTTGGAGAA 960
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 181 AATGCAATGCTATTGCACAGGTTCAATGCACTGATATGACTGCCGAACTTGGAGAA 240
 QY 961 GAGCTTGAGAGAAATCTTGCAACCATTTCCGTTAGGAGATATGCGCCACACAGGAA 1020
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 241 GAGCTTGAGAGAAATCTTGCAACCATTTCCGTTAGGAGATATGCGCCACACAGGAA 300
 QY 1021 GTTCAGGTTGGTTCAGTTCTGCGCCCTTAACCCCGCAGCTAGCTATATGACTGGACAG 1080
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 301 GTTCAGGTTGGTTCAGTTCTGCGCCCTTAACCCCGCAGCTAGCTATATGACTGGACAG 360
 QY 1081 GTGCTTACAATTCAGGAGGATGTAATGTAAGATTGAGTTGAGTTGACTGATGCACTTCTA 1140
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 361 GTGCTTACAATTCAGGAGGATGTAATGTAAGATTGAGTTGAGTTGACTGATGCACTTCTA 420
 QY 1141 CTTTGTGCTGAGCAATTAATG 1160
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 421 CTTTGTGCTGAGCAATTAATG 440

RESULT 12
 CB604576/c
 LOCUS
 DEFINITION 3529.1.61.1.C02.X.1 3529 - 2 mm ear tissue from Schmidt and Hake
 lab's Zea mays cDNA, mRNA sequence.
 ACCESSION CB604576
 VERSION CB604576.1 GI:29544196
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 578)
 Walbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 JOURNAL Unpublished
 CONTACT Walbot V
 DEPARTMENT Department of Biological Sciences
 INSTITUTION Stanford University
 ADDRESS 855 California Ave, Palo Alto, CA 94304, USA
 TEL 650 723 2227
 FAX 650 725 8221

Email: walbot@stanford.edu
 Plate: 3529.1.61.1 row: C column: 02.
 FEATURES
 source
 1. 578
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /tissue_type="ear"
 /dev_stage="2 mm"
 /lab_host="E. coli XLOLR"
 /clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake
 labs"

/note="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI;
 Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu
 amplified. Ampicillin is the selection marker."
 BASE COUNT 164 a 145 c 103 g 166 t
 ORIGIN

Query Match 32.4%; Score 430; DB 14; Length 578;
 Best Local Similarity 100.0%; Pred. No. 4e-51;
 Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 742 ACAAAGTAATGATGATGAAAAAGAGAAAGGAAAAATATCAACATTGCTCTGTAGTTGGT 801
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 527 ACAAAGTAATGATGATGAAAAAGAGAAAGGAAAAATATCAACATTGCTCTGTAGTTGGT 468
 QY 802 CTTACTGCAATGTTGGCCAAAGCTAATATATAGCCAGCCAGGCTGGAGTGTATGTTTC 861
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 467 CTTACTGCAATGTTGGCCAAAGCTAATATATAGCCAGCCAGGCTGGAGTGTATGTTTC 408
 QY 862 ACAAACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCAACA 921
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 407 ACAAACAGTTGCCAGGAGTATGCAAGCAGAAATATCAATGTGAATGCTATTGCAACA 348
 QY 922 GGGTTTCATTGTCATCTGATATGACTGCCGAACCTTGAGAGAGAGCTTGAGAGAAATCTTG 981
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 347 GGGTTTCATTGTCATCTGATATGACTGCCGAACCTTGAGAGAGAGCTTGAGAGAAATCTTG 288
 QY 982 TCAACCAATTCGGTTAGGAGATATGGCCAAACAGAGGAAGTTGCGAGGTTGTCGAGTTC 1041
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 287 TCAACCAATTCGGTTAGGAGATATGGCCAAACAGAGGAAGTTGCGAGGTTGTCGAGTTC 228
 QY 1042 CTGSCCCTTAACCCCGCAGCTAGCTATATGCTGGAAGGTTGCTTACAATGACGAGGG 1101
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 227 CTGSCCCTTAACCCCGCAGCTAGCTATATGCTGGAAGGTTGCTTACAATGACGAGGG 168
 QY 1102 ATGCTAATGTAAGATTGAGTTAGCTTATGCTGACCTTCTTACCTTTGCTGAGCAATTAATGT 1161
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 167 ATGCTAATGTAAGATTGAGTTAGCTTATGCTGACCTTCTTACCTTTGCTGAGCAATTAATGT 108
 QY 1162 TGAACACCCCT 1171
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 107 TGAACACCCCT 98

RESULT 13
 BU098345
 LOCUS
 DEFINITION 946134D10.Y1 946 - tassal primordium prepared by Schmidt lab Zea.
 mays cDNA, mRNA sequence.
 ACCESSION BU098345
 VERSION BU098345.1 GI:22545986
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 648)
 Walbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL
COMMENT

Unpublished

Contact: Walbot V
Department of Biological Sciences
Stanford University
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Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946134 row: D column: 10.

FEATURES
source

1. .648
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
/db_xref="taxon:4577"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to inflorescence development"
/lab_host="XLOLR"
/clone_lib="946 - tassels primordium prepared by Schmidt lab"
/note="Organ: tassels; Vector: HybriZAP; Site 1: EcoRI; Site 2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
164 a 159 c 184 g 141 t

Query Match 30.0%; Score 398; DB 13; Length 648;
Best Local Similarity 99.5%; Pred. No. 9e-47;
Matches 548; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 220 GCCGGGGCGCGCGCTCCCGCGGGGTTCGTCAGTTGGTGGAGGCGCGCGCGC 279
DB 83 GCCGGGGCGCGCGCGCTCCCGCGGGGTTCGTCAGTTGGTGGAGGCGCGCGC 142
QY 280 TTCTCTCCAGCTCGGTCGCGCGCGGTTCCTGTGTGCAACCCATGTTGCTGCT 339
DB 143 TTCTCTCCAGCTCGGTCGCGCGCGGTTCCTGTGTGCAACCCATGTTGCTGCT 202
QY 340 GTTGAAACAGAGTTGTAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 399
DB 203 GTTGAAACAGCAATTGTAAGATGCTACCAAGCTGGAAGCTCCAGTTGTTGTTTACA 262
QY 400 GGTGCATCTAGAGGATTGTAAGCAACTGCTAGCCCTTGGAAAGCAGGATGCAAG 459
DB 263 GGTGCATCTAGAGGATTGTAAGCAACTGCTAGCCCTTGGAAAGCAGGATGCAAG 322
QY 460 GTTCTGTAAACTATGCCCGGTCTCGAAAGAGGCTGAAGAGTCTCCAAAGAGATTGAA 519
DB 323 GTTCTGTAAACTATGCCCGGTCTCGAAAGAGGCTGAAGAGTCTCCAAAGAGATTGAA 382
QY 520 GCATCTGTGTGAGGCTATCACTTCGAGAGAGATGTTCAAAGAGCTGATGATGAG 579
DB 383 GCATCTGTGTGAGGCTATCACTTCGAGAGAGATGTTCAAAGAGCTGATGATGAG 442
QY 580 TCTATGTAAGAGAGCTAGATAAATGGGGAACAATAGATGCTGTTAAATAATGCA 639
DB 443 TCTATGTAAGAGAGCTAGATAAATGGGGAACAATAGATGCTGTTAAATAATGCA 502
QY 640 GGGATTACACGAGACATGTTGATGAGGATGAAGAAATCTCAGTGCAGAGCTAATT 699
DB 503 GGGATTACACGAGACATGTTGATGAGGATGAAGAAATCTCAGTGCAGAGCTAATT 562
QY 700 GATCTGAATCTTACGGGCTTTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAA 759
DB 563 GATCTGAATCTTACGGGCTTTCTTTGTACACAGGCTGCAACAAAAGTAATGATGAA 622
QY 760 AAGAGAAAGG 770
DB 623 AAGAGAAAGG 633

RESULT 14
BM737475/cLOCUS
DEFINITION

952056D06.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea
mays cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 952056 row: D column: 06.

Location/Qualifiers

1. .589

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="BMS (Black Mexican Sweet)"

/db_xref="taxon:4577"

/tissue_type="suspension culture"

/dev_stage="mixed logarithmic and stationary growth phases"

/lab_host="DH10B"

/clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"

/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

Score

Pred. No.

2.6e-46;

29.8%;

395;

DB 12;

Length 589;

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 Qy 520 GCATCTGGTGGGAGGCTATACCTTCGAGAGAGATGTTTCAAAAGAGCTGATGTAGAG 579
 Db 240 GCATCTGGTGGGAGGCTATACCTTCGAGAGAGATGTTTCAAAAGAGCTGATGTAGAG 181
 Qy 580 TCTATGATCAAGACAGCTCTAGATAAATGGGAAACAATAGATGCTGTGTAATAATGCA 639
 Db 180 TCTATGATCAAGACAGCTCTAGATAAATGGGAAACAATAGATGCTGTGTAATAATGCA 121
 Qy 640 GGGATTACACGAGACACATGTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAATT 699
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 Qy 700 GATCTGAATCTTACTGG 716
 Db 60 GATCTGAATCTTACTGG 44

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 mayes cDNA, mRNA sequence.
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 VERSION BE510480.1 GI:9731728
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 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 626)

REFERENCE Zea mays
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL University
 COMMENT Unpublished
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946053 row: B column: 11.
 Location/Qualifiers
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 inflorescence development"
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 lab"

FEATURES
 source
 136 a 169 c 175 g 146 t
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 ORIGIN
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 Best Local Similarity 99.6%; Pred. No. 2.4e-46;
 Matches 495; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 220 GCCGGGCGCGCGCGCTCCCGCGGGGTTCGTACGTTTGGTGGAGGCGCGCGCGC 279
 Db 114 GCCGGGCGCGCGCGCTCCCGCGGGGTTCGTACGTTTGGTGGAGGCGCGCGCGC 173

Search completed: November 7, 2003, 19:33:22
 Job time : 3157 secs

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 Db 174 TTCTCTCCACGCTGCGGTCCGCGGTCTCTGTGTGCAAAACCCATGTTCTGTCT 233
 Qy 340 GTTGAACAAGCAGTTGTAAGAAGATGCTACCAAGCTGGAGCTCCAGTTGTTGTTTACA 399
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 Qy 400 GGTGCATCTAGAGGATGTTGTAAGCAACTGCTCTAGCCCTTGGAAAAAGCAGGATGCAAG 459
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 Qy 460 GTTCTGGTAAACTATGCCCCGCTCTCGAAAAGAGGCTGAAGAGTCTCCAAAGAGATTGAA 519
 Db 354 GTTCTGGTAAACTATGCCCCGCTCTCGAAAAGAGGCTGAAGAGTCTCCAAAGAGATTGAA 413
 Qy 520 GCATCTGGTGTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGAGCTGATGTAGAG 579
 Db 414 GCATCTGGTGTGAGGCTATCACCTTCGGAGGAGATGTTTCAAAAGAGCTGATGTAGAG 473
 Qy 580 TCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGCTGCTAAATAATGCA 639
 Db 474 TCTATGATGAAGCAGCTCTAGATAAATGGGAAACAATAGATGCTGCTAAATAATGCA 533
 Qy 640 GGGATTACACGAGACACATGTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAATT 699
 Db 534 GGGATTACACGAGACACATGTTGATGAGGATGAAGAAATCTCAGTGGCAAGACGTAATT 593
 Qy 700 GATCTGAATCTTACTGG 716
 Db 594 GATCTGAATCTTACTGG 610